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Development of Breast Cancer

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14. ABSTRACT The purpose of this project is to identify effector molecules that act as a link between cell proliferation, cell survival and chromosomes stability. We have hypothesized that chromosomal segregation and apoptotic pathways are linked and have a role in breast cancer. Rad21 is one of the major cohesin subunits that holds sister chromatids together until anaphase, when proteolytic cleavage by separase allows chromosomal separation. Our study demonstrates that in contrast to described functions of Rad21, in chromosome segregation and DNA repair, cleavage of the cohesion protein and translocation of the C-terminal cleavage product to the cytoplasm are early events in the apoptotic pathway that amplify the apoptotic signal in a positive feed back manner by activating more Caspases. Overexpression of the c-terminal cleavage products results in apoptosis in MCF-7 breast cancer cells. Given the role of hRad21 in chromosome cohesion, the cleaved C-terminal product and its translocation to the cytoplasm may act as a nuclear signal for apoptosis. Furthermore, hRad21 is differentially expressed in human breast tumors and in breast cancer derived cell lines in comparison to normal breast epithelial cells. Future studies will identify the protease that cleaves Rad21 and evaluate hRad21 as a prognostic marker for breast cancer development.					
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Table of Contents

Cover.....	1
SF 298.....	2
Table of Contents.....	3
Introduction.....	4
Body.....	4
Key Research Accomplishments.....	9
Reportable Outcomes.....	10
Conclusions.....	10
References.....	11
Appendices.....	13
Appendix-I (Work accomplished)	13
Appendix-II Bibliography	15
Appendix-III List of Personnel	16
Appendix-IV (Published Manuscript)	17

Introduction

One of the hallmarks of cancer cells is a decrease in or resistance to cell death coupled with an increase in cell proliferation. In particular, cancer cells can resist conventional chemotherapeutic agents by evading apoptosis. Therefore, a mechanistic understanding of the processes that link cell proliferation and cell death will provide important knowledge in the treatment of cancer. Cell death by apoptosis plays an essential role in normal development and physiology in the breast (Jacobson et al., 1997) as well as in the development of breast Cancer (Schedin et al., 1996; Wu, 1996). The degree of apoptosis can be an important factor in both the progression of breast cancer and the response to treatment (Furth, 1999; Lipponen, 1999). A high apoptotic index (number of apoptotic cells per square millimeter of neoplastic tissue) is related to malignant cellular features and is an indicator of invasiveness and cell proliferation in breast cancer (Lipponen, 1999). The response to treatment of breast cancer is improved by increasing the percentage of cells undergoing apoptosis. Thus, cell cycle progression and control of apoptosis are thought to be intimately linked processes. Mitosis and apoptosis are closely interrelated (Lipponen et al., 1994). Although proteins that regulate apoptosis have been implicated in restraining cell cycle entry (Hauf et al., 2001) and controlling ploidy (Minn et al., 1996), the effector molecules at the interface between cell proliferation and cell survival have remained elusive. **The purpose of the study is to identify the effector molecules that act as a link between cell proliferation, cell survival and chromosomal stability. We have hypothesized that chromosomal segregation and apoptotic pathways are linked and have a role in the development of aneuploidy in breast tumors. Human Rad21, a protein that establishes and maintains sister chromatid cohesion during mitosis, may provide a link between cell division and cell death: and cleavage of Rad21 may signal subsequent events of cell death including DNA degradation. We also hypothesize that hRad21 helps maintain chromosomal stability in mammary cells and its dysregulation results in breast cancer formation.** To test these hypotheses we have the following **specific aims**: 1) evaluate the role of hRad21 in the apoptotic response and the role of apoptotic proteins on cleavage of hRad21; and 2) determine the expression and localization of hRad21 protein and mRNA in normal and malignant breast carcinoma cell lines and tumor specimens with known levels of aneuploidy.

Following is the final report for this project that includes a no cost extension for the period of July 1, 2004-June 30-2005. We have completed the first technical objective (role of Rad21, in apoptotic response) and have made substantial progress in the second objective (Rad21 expression in breast tumors). Over the last year, with limited resources we just focused on the characterization of the protease that cleaves Rad21 during apoptotic response. Our other focus was to prepare and submit grant proposals to seek funding to continue this line of research. We have been successful in both of these goals. Our research indicates the presence of a novel Rad21 protease in the nucleus, which remains to be identified. I have secured funding from NIH to carry out the identification and characterization of this novel Rad21 protease.

In summary, the research carried out as the part of this IDEA award indicates that in addition to establishing and maintaining sister chromatid cohesion during mitosis, hRad21 plays a direct role in apoptosis, and its cleavage during apoptosis by a novel protease act as a nuclear signal to initiate cytoplasmic events involved in the apoptotic pathway. A manuscript describing this work (see Appendix IV) was published in the *Journal of Molecular and Cellular Biology* (Pati et al., 2002), one manuscript is under revision and two more manuscripts are in preparation. In accordance with the approved statement of work, tasks for technical objective 1 and 2 have been completed (Appendix 1).

Body of the report

Rad21 is one of the major cohesin subunits that holds sister chromatids together until anaphase, when proteolytic cleavage by separase, a caspase-like enzyme, allows chromosomal separation (Uhlmann et al., 1999; Biggins and Murray, 1999; Hauf et al., 2001). **Rad21 plays a critical role in the eukaryotic cell division cycle by regulating sister chromatid cohesion and separation at the metaphase to anaphase transition (Ciosk et al., 1998; Michaelis et al., 1997; Nasmyth et al., 2000).** However, in addition to its role in chromosomal segregation, cohesins can associate with different sets of proteins to achieve diverse functions, including regulation of gene expression, DNA repair, cell cycle checkpoints and centromere organization (for a review see Hagstrom and Meyer, 2003). Surprisingly, work from ours and others have indicated that not only cohesin Rad21 plays a critical role in mitosis, it can also induce apoptosis (Pati et al., 2002, Chen et al., 2002).

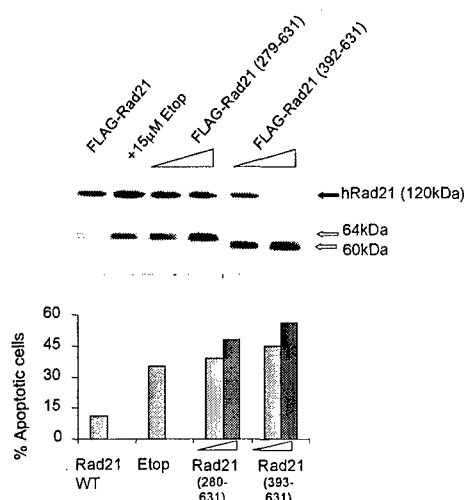


Fig. 1. Induction of cell death by cleaved Rad21 proteins (Rad21 280-631 and Rad21 393-631). Molt4 T-cells were transiently transfected with the plasmids encoding Rad21 WT (3 μ g) or C-terminal cleavage products (3 and 6 μ g), together with 3 μ g of red fluorescent protein (RFP) expression plasmids. Total plasmid (9 μ g) for each transfection was kept constant to avoid promoter competition. Forty-eight hours following transfection, RFP positive cells were evaluated by microscopy, and the percentage of RFP-positive cells with apoptotic morphology was estimated based on a count of 300 cells (Etop, etoposide).

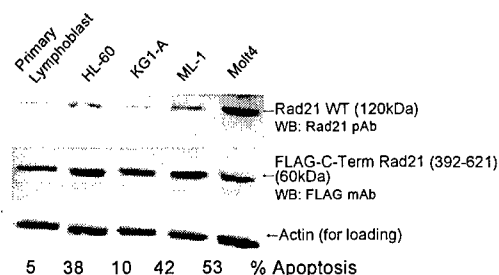


Fig. 2. Endogenous status of Rad21 protein influences C-terminal Rad21-induced apoptosis in normal lymphoblasts and myeloid leukemia cells. Cells were transfected with FLAG-tagged Rad21 together with an RFP expression plasmid using a combination of nucleofection (Amagx Inc, Gaithersburg, MD) and lipid based transfection reagents from Qiagen (Valencia, CA) and Bio-Rad (Hercules, CA). Transfection efficiency was 15%-20%. 48 h posttransfection, lysates were prepared and analyzed in Western blots using Rad21Ab, FLAG M2 mAb, and actin antiserum. A sample of RFP-positive cells were evaluated by microscopy, and the percentage of RFP-positive cells with apoptotic morphology was estimated by counting 300 cells.

Little is known about the role of Rad21 in human malignancies. We have characterized the role of Rad21 in apoptosis and have evaluated the expression of Rad21 in 800 human breast tumor specimens to identify its role in breast cancer progression.

Aim 1) Role of Rad21 in apoptotic response: Tasks completed as parts of this objective clearly demonstrate a role of hRad21 in the apoptotic response and cleavage of the hRad21 protein in human cells by a Caspase-like activity. Our published and recent unpublished studies demonstrate, that Rad21 is cleaved during apoptosis at two unique sites (Asp residue 279 and Cysteine residue 392) and that the C-terminal cleavage products translocate to the cytoplasm where it enhances apoptosis. Moreover, overexpression of C-terminal Rad21 (280-631aa and 393-631aa) in the cytoplasm of apoptosis sensitive (e.g. MCF-7, Molt4) or resistant (293 cells) cell lines induces apoptosis in contrast to expression of full length or N-terminal (1-279aa) Rad21. Analysis of transfected 293T and Molt4 cells by multiple apoptosis assays, including cellular morphology under light microscopy and staining with TUNEL, Annexin V and DAPI, clearly indicate the ability of the 64-kDa C-terminal hRad21 to induce apoptosis. Using similar experimental approaches, we have now tested the effect of the 60-kDa hRad21 fragment (aa 393-631) on apoptosis. We found that like that of the 64-kDa Rad21, the 60-kDa Rad21 C-terminal fragment is also highly apoptotic. Quantitative analysis of Molt4 T-cells transfected with C-terminal hRad21 (aa 280-631 or aa 393-631) plasmids showed a dramatic increase in nuclear degradation compared with cells expressing wild-type hRad21 (pFLAG Rad21) (Fig. 1). The level of apoptosis in cells expressing the 60- or 64-kDa fragment is comparable to Molt4 cells treated with 15 μ M etoposide for 6 h. In these cells, apoptosis was assayed by monitoring the phenotype of the DAPI-stained nuclei. Cells transfected

with hRad21 C-terminal plasmids had considerably higher concentrations of cellular and nuclear phenotypes typical of apoptosis, such as having a round appearance with shrunken cell volume, chromatin condensation, and nuclear disintegration, than did cells with intact hRad21WT constructs.

Results indicate the proapoptotic activity of the C-terminal Rad21 fragments appears to rely on the endogenous status of Rad21 protein (Fig. 2). For example, when overexpressed, both the C-terminal fragments of Rad21 (60 kDa [Fig. 2, panel 2] and 64 kDa, [data not shown]) induce apoptosis in tumor cells with higher endogenous Rad21 levels (e.g., myeloid leukemia cells Molt4, ML-1, and HL60), while primary lymphocytes and tumor cells with low Rad21 expression (e.g. KG1A cells) are resistant, thus making Rad21 protein status an ideal target for therapy. This phenomenon may be due to:

- (a) a hyperactive export mechanism that regulates the translocation of the proapoptotic Rad21 C-terminal fragment to the cytoplasm in Rad21 overexpressed cells or
- (b) an overactive Rad21-specific protease in cells with a high level of Rad21, resulting in higher Rad21 cleavage and translocation to cytoplasm.

We have further examined the importance of the proteolytic cleavage of Rad21 during apoptosis by engineering a Rad21 construct in which the endogenous apoptotic cleavage site is replaced by the TEV protease recognition sequence (TEV-Rad21). Expression of TEV-Rad21 alone had no effect on the cell cycle, where as co-expression of TEV-Rad21 with the highly specific TEV protease induced apoptosis in Jurkat and 293 cells (Fig. 3). In this assay, inclusion of TEV recognition site to other parts of Rad21 had no effect (data not shown). Thus,

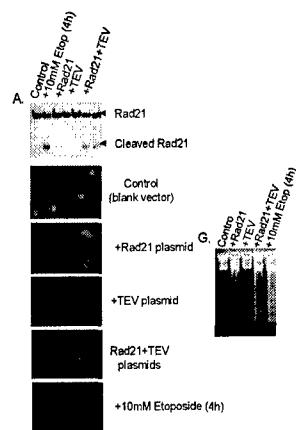


Fig. 3: Cleavage of an engineered Rad21 that replaces the apoptotic cleavage site at Asp²⁷⁹ with a TEV protease recognition motif can induce apoptosis in Jurkat T cells. A Western blot analysis (A) of Jurkat cells (profiled in B through F) using Rad21 monoclonal antibody. Jurkat cells were transfected with blank vectors (B), treated with Rad21-engineered plasmid that replaced its apoptotic cleavage site with a TEV protease recognition sequence (C), treated with TEV expression plasmid (D), or treated with both Rad21 and TEV expression plasmids (E). As a control, cells were also treated with 10 μ M etoposide for 4 h to induce apoptosis (F). Thirty-six hours following transfection, cells were fixed, stained with DAPI, and visualized using fluorescence microscopy. Transfection efficiency was 30%-40%. Assay of DNA fragmentation during Rad21 cleavage in Jurkat cells was also performed (G). In an identical set of experiments, cells were harvested and genomic DNA extracted from the cells and analyzed by 1.8% agarose gel electrophoresis. The DNA was visualized by UV illumination after Cyber Gold staining (Molecular Probes, Eugene, OR).



Fig. 4: Caspase 3 and 7 are not essential for the cleavage of hRad21. In vitro translated unlabeled (nonisotopic) Rad21 in wheat germ extract was incubated in the presence of MCF-7 whole cell lysate (no treatment) (left lane) or lysates that were immunodepleted using caspase 7 antibody from cells transfected with caspase 7 siRNA for 96 h and challenged with 60- μ M etoposide, 6 h before harvest (lanes 2 and 3). Samples were resolved in 4%-20% gradient SDS-PAGE gel and immunoblot analyses were performed using caspase 7 and Rad21 monoclonal antisera. MCF-7 cells used here lack caspase 3.

cleavage of Rad21 close to its endogenous, apoptotic cleavage site is sufficient to induce apoptosis in both apoptosis sensitive and resistant cells. *In vitro* cleavage assays have indicated that caspase-3 and -7 can cleave Rad21. However, we recently have shown, that Rad21 can be cleaved in Caspase-3 deficient MCF7 cells in which Caspase-7 activity is blocked by siRNA/antibody treatment (Fig. 4).

Since Rad21 is a nuclear protein and the cleavage initially occurs in the nucleus, the protease that cleaves Rad21 may reside inside the nucleus. Caspase-2 is localized in nucleus (Shikama et al., 2001), but it cannot cleave Rad21 *in vitro* (Chen et al., 2002). These findings suggest the presence of a novel caspase or caspase-like molecule in the nucleus that cleaves Rad21 early in apoptosis. However, the physiological protease that cleaves Rad21 during apoptosis and the mechanisms by which apoptosis is promoted remains at present elusive.

Feasibility of the purification scheme to identify the protease that cleaves Rad21. To identify the physiological protease that cleaves Rad21 in the nucleus early in apoptosis, we undertook a set of pilot studies using Mono Q, an anion-exchange column, to isolate the enzymatically active fractions based on surface charge of the molecule, along with a BioLogic DuoFlow chromatography system (Bio-Rad, Hercules, CA). A Mono Q column contains quaternary amine groups and thus has a positive charge.

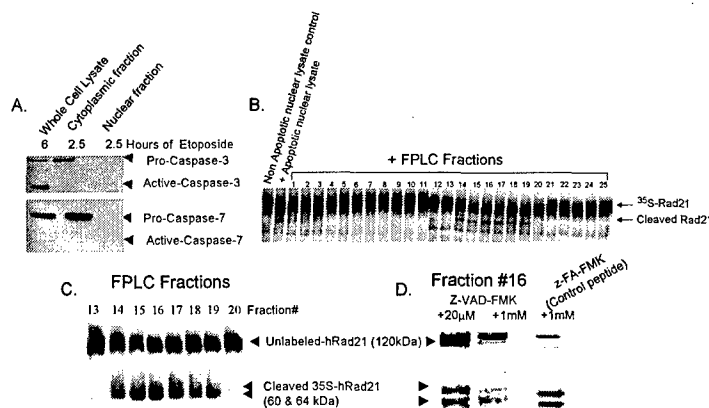


Fig. 5: Biochemical purification of active protease fractions that cleave hRad21 *in vitro* from nuclear lysates of Molt4 cells undergoing early apoptosis (10 μ M etoposide treatment for 2.5 h), using preparative FPLC on a Mono Q column: (A) Assay for caspases 3 and 7 contamination of the nuclear fraction used for FPLC using Western blot analysis. Whole cell lysates (lane 1) from Molt4 cells treated with 10 μ M etoposide for 6 h are shown as positive controls along with cytoplasmic fractions (lane 2). (B) In vitro translated ³⁵S-hRad21 in the rabbit reticulocyte lysates were incubated with nuclear lysates from Molt4 cells treated without etoposide (lane 1) and with 10 μ M etoposide for 2.5 h (lane 2). Shown right are the FPLC-purified fractions of apoptotic nuclear lysates. Samples were resolved on a 12.5% SDS-PAGE gel, fixed with methanol and acetic acid for 30 min, dried on a gel dryer, and exposed to a Storm imager. (C) Cleavage of in vitro translated unlabeled (nonisotopic) hRad21 in wheat germ extracts by FPLC fractions 13-20. Samples were analyzed on an SDS-6% PAGE gel followed by Western blotting with hRad21 C-terminal pAb. (D) In vitro cleavage of unlabeled-Rad21 by FPLC fraction 16 in the presence of a broad-spectrum caspase inhibitor Z-VAD-FMK (20 μ M and 1 mM) or a peptide control Cbz-Phe-Ala-fluoromethyl ketone (z-FA-FMK) (1 mM).

Caspases are negatively charged molecules and should bind to the Mono Q column. In this experiment, 3 L of Molt4 cells were treated with 10 μ M etoposide for 2.5 h. Quantitative measurement of early apoptosis was performed by staining a sample of cells following etoposide treatment with Annexin V as previously described (Pati et al., 2002). Isolation of nuclei was based on osmotic shock followed by sucrose gradient centrifugation. The

quality and density of the nuclei were monitored by staining of the nuclear material with DAPI and visualization using a hemocytometer. Our lab uses this method routinely to prepare nuclei from Molt4 cells with high purity (Pati et al., 2002). The purity of the nuclear fraction was verified in a Western blot using nuclear lamin and cytoplasmic tubulin antibodies and was found to be pure with no detectable cytoplasmic contamination (Pati et al., 2002). Although Western blot analysis was used to identify contamination of the nuclear preparations with cytoplasmic caspase 3 and caspase 7, two major apoptotic proteases, contamination was not detected (Fig. 5A).

Fast-performance liquid chromatography (FPLC) was used to purify nuclear lysates from early apoptotic Molt4 cells. Nuclear protein (500 mg at 1000 mg/ml) in buffer consisting of 10 mM Tris-HCL, 0.1 mM EDTA, 1 mM DTT (pH, 7.5), and 0.2 mM PMSF (buffer A) was applied to the Mono Q column, which had been equilibrated and developed with the same buffer. Then 0.75-ml fractions were collected and the enzymatic activity was tested in an in vitro ³⁵S-Rad21 cleavage assay as described previously (Pati et al., 2002). As shown in Fig. 5B, in vitro translated Rad21 was cleaved by the Molt4 nuclear lysates that were treated for 2.5 h with 10 μ M etoposide (lane 2). However, control lysates treated solely with vehicle failed to cleave Rad21 in the cleavage assay (lane 1). FPLC fractions 14-19 were able to cleave Rad21 in the in vitro cleavage assay indicating the presence of active enzyme fractions, and the intensity of the cleavage bands' peak in fractions 16 and 17. We confirmed these findings using fractions 13-20 to cleave Rad21 employing in vitro translated unlabelled hRad21 in wheat germ extracts and assaying the cleavage in Rad21 immunoblots (Fig. 5C). The broad-spectrum caspase inhibitor z-VAD-FMK, but **not** the control peptide z-FA-FMK, could inhibit the cleavage of the 64-kDa hRad21 fragment by FPLC fraction 16 at higher doses (1 mM), but it had no effect on the 60-kDa fragment (Fig. 5D). Because these findings suggest the involvement of a novel caspase-like protease, they support the hypothesis that a nuclear protease cleaves Rad21 early in apoptosis and can be isolated.

In future the identification and characterization of this novel protease should be carried out. Identification of this protease not only will shed light on the nuclear signal that initiates apoptosis, will also provide a ideal target for therapeutic intervention. These experiments were instrumental in identifying if Rad21 cleavage is essential for induction of apoptosis and/or sensitizes cells to undergo apoptosis after exposure to apoptotic agents.

Sequence mining indicates that a region of 104 amino acid residues in C-terminal Rad21 has high consensus (26% identities, 43% positives) with the sequence upstream of the death domain (DD) of several apoptosis related proteins (Fig. 6), such as Tumor Necrosis Factor (TNF) receptor super family, apoptosis inducing receptor TRAIL-R2, and apoptosis inducing protein/death receptor 5 (Schneider et al 1997, Screaton et al 1997, Sheridan et al 1997, Walczak et al 1997). However, the functional significance of this domain in apoptosis-inducing proteins is not known. TNF receptor superfamily members have DD and their involvement in apoptosis requires TNF signaling from outside of the cell. C-terminal Rad21 does not have a death domain. It is currently not known whether C-terminal Rad21 induced apoptosis requires extracellular signals, like those in the TNF superfamily. **The conserve sequence between C-terminal Rad21 and TNF receptor superfamily members implies that Apoptosis induced by C-terminal Rad21 and the tumor necrosis factor (TNF) receptor superfamily may share part of the common apoptotic pathway.**

Rad21	QGLZHLMDENINVS	EGGDS	FLSVDF	SPMPTM	QQT	VNEERAFAL	LE	IDITVR	TKAKR	EF	IVDS	VKELDS	SK	LAQLS	YEL	IV	TTLDLA	PTKRI						
AIP	RECAP	INVLI	HY	SILC	TQV	QEMEV	EPAEF	GVNM	SG	SHL	LE	A-----	AERSC	RRLL	PF	NEGDP	EL	QCFC	FADL	PFDSWE	LMRK			
consensus	+	P+	+D	++	VS+	P	P+	V+		T	L	P	E	E	LEP		E	+R+L+V	+		+T+R	D++D+V	P	+KL

Fig.6 Homology of C-terminal human Rad21 (amino acids 257-360) with apoptosis-inducing proteins (AIP) that include tumor necrosis factor receptor superfamily (member 10b, amino acids 188-286), apoptosis inducing receptor TRAIL-R2 (amino acids 263-361), and apoptosis inducing protein/death receptor 5 (amino acids 234-332). All these apoptosis-inducing proteins have a region with the same amino acid sequence.

To characterize the role of this identified AIP domain in C-terminal Rad21, we have set up a Hela Tet-On gene expression systems conditionally expressing Rad21 full length, Rad21(1-282aa), Rad21(281-631aa) and Rad21(253-631aa). Gene expression in Tet-on system is turned on by adding doxycycline and is tightly regulated in response to varying concentrations of doxycycline. These inducible cell lines are important reagent to study the C-terminal Rad21 stimulated apoptosis. We have also generated similar systems for the MCF7 breast cancer cell line, which will be used in testing C-terminal Rad21-induced apoptosis in breast cancer cells and will provide a valuable tool to probe the apoptotic activity of Rad21.

Aim 2) Expression and localization of Rad21 Protein and mRNA in normal and malignant breast carcinoma cell lines and tumor samples:

We have examined the expression pattern of Rad21 message and protein in a variety of breast cancer cell lines (MCF7, MDA-MB-157, MDA-MB-231, MDA-MB-436, BT-20, HBL100, and SKBR-3). In these cells, Rad21 appeared to have altered expression patterns. Compared to normal human mammary epithelial cells (H-MEC), Rad21 mRNA is overexpressed in all the cells tested, except for BT20, where its expression was found to be considerably down regulated. However, subsequent Southern blot analysis of the genomic DNA from the breast cancer cell lines didn't reveal any defects in Rad21 gene structure. Expression and localization of the hRad21 protein in normal and malignant breast cancer cells were performed using immunocytochemistry and immunofluorescence techniques. hRad21 efficiently localizes to the nucleus of various mammalian cells assayed by immunofluorescence staining using either the affinity purified polyclonal or monoclonal hRad21 antibodies, developed by us.

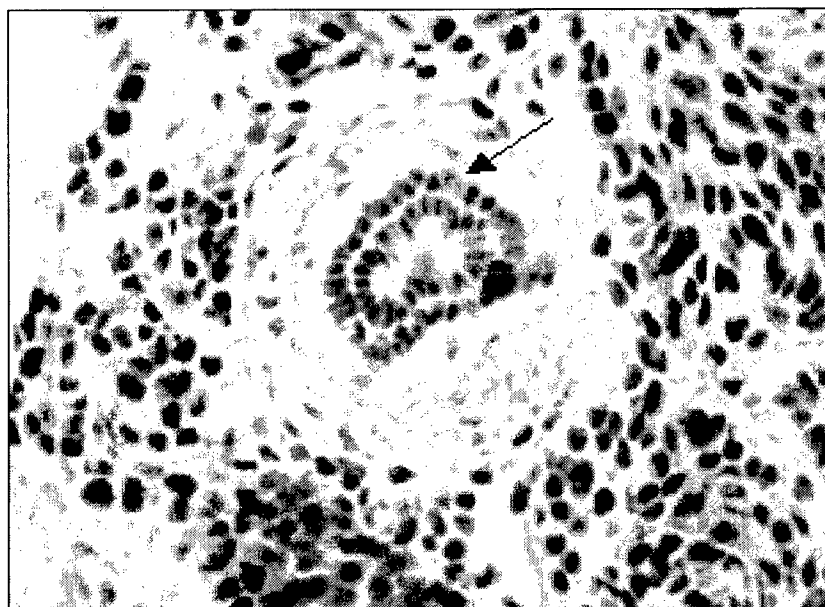


Fig. 7: Immunohistochemical staining of Rad21 in human breast tumor specimen. The signal was developed using 3,3'-diaminobenzidine chromogen (brown) with a methyl green counter stain. In the center shows normal tissue (arrow). X100 magnification.

To further characterize the contribution of Rad21 to tumor localization of Rad21 protein, we used immunohistochemistry (Allred et al., 1993; Berardo et al., 1998) in 800 human breast tumor specimens with known status for aneuploidy, estrogen receptor, and a number of other markers with appropriate controls available from the Allred lab at the Baylor Breast Cancer Center. The Allred lab has assisted us in developing a robust assay to immunolocalize the hRad21 protein using monoclonal hRad21 antibody. Since most referral specimens are fixed 10% neutral buffered formalin and processed at variable rates and times, increased sensitivity and standardization of the assay is achieved through the use of heat induced antigen retrieval post-deparaffinization. Endogenous nonspecific protein blocking then follows. Subsequently, incubation with the primary antibody (monoclonal hRad21) is performed, followed by a biotinylated secondary antibody incubation directed against the mouse. These are then followed by incubation in horseradish peroxidase (HRP)-labeled streptavidin, which then binds to the biotin label of the secondary antibody. The entire reaction is then visualized by incubation with 3,3 diaminobenzidine which, in the presence of HRP, produces a brown reaction product at the site of the antigen-antibody interaction. Enhancement of the reaction product is achieved by the addition of the heavy metal osmium tetroxide, which increases the tone of the reaction product and elevates the signal: noise ratio of the assay. Scoring of immunostained slides for hRad21 expression is performed by the PI in a blinded way according to the protocol described for Bcl-2 expression in breast tumor specimens (Berardo et al., 1998) and based on the proportion of cells staining positive, described by the Allred laboratory. Statistical analysis of these samples have been completed by the statistics core

(S.G. Hilsenbeck and C.C. Chenault) of the Breast Center at Baylor College of Medicine. Analysis indicates aberrant expression of Rad21 in human breast tumors. For an example, in one set of tumors Rad21 is highly overexpressed while in another set its expression is completely absent. There appears to be a high correlation between Rad21 expression in tumor and adjacent cells. Typically, Rad21 find to be expressed higher in infiltrating breast cancer (IBC) than in normal. The p value ($P < 0.001$) indicated a highly significant difference. No obvious association was noted between ploidy of tumor and Rad21 expression in tumor tissues. However, it appears that there is an association between tumor ploidy and the expression of Rad21 in adjacent normal tissues that is statistically significant. There is a modest association between Rad21 and ER positivity in IBC but not in normal tissue. There was no significant association between Rad21 expression with cathepsin-D, her2-neu and EGFR. Due to lack of availability of enough sample materials, we were not able to perform the TUNEL assay as proposed to correlate the apoptotic index with Rad21 expression in these specimens. Based on these results, in future studies Rad21 can be evaluated as a potential candidate prognostic marker for breast cancer progression.

Due to difficulty in isolating RNA from frozen tumor specimens, expressions of *hRAD21* mRNA was being investigated in a subset of 10 breast tumors with Northern blot analysis. However, due to poor quality of the RNA, Northern analysis of Rad21 expression was not successful. The LOH studies (technical objective 2B) were proposed in collaboration with Dr. Peter O'Connell. This collaboration could not materialized partly due to the relocation of the O'Connell lab and partly due to lack of samples. Hence, this sub-aim was not pursued.

As described above, studies in over 800 human breast tumor specimen indicate that Rad21 is significantly overexpressed in human breast cancer cells in comparison to normal cells (Fig. 7, Zhang, Allred and Pati, manuscript in preparation), making it an attractive candidate for the adoptive immunotherapy with antigen-specific cytotoxic T-lymphocytes (CTL). Rad21 has also been reported to be amplified in prostate cancer (Porkka et al., 2004). Rad21 is a potential tumor-associated self antigen similar to survivin, telomerase and MDM2 (Gordan et al., 2002). CTL specific for survivin and telomerase have been generated by several groups indicating that CTL can be successfully generated against self-antigens. Moreover, studies with survivin-specific CTL have shown that only tumor cells overexpressing survivin are recognized by CTL in contrast to non-malignant cells, like hematopoietic stem cells that express survivin at low levels (Pisarev et al., 2003). Thus, we hypothesize that Rad21-specific CTL will only recognize Rad21 overexpressing malignant cells. Sofar the immune response to Rad21 has not been studied and we have recently secured seed funds from the Baylor Cancer Center to generate Rad21-specific CTL for the adoptive immunotherapy of Rad21 positive breast cancer.

Key Research Accomplishments

- Human Rad21 (hRad21) cohesin is cleaved at residue Asp (D)²⁷⁹ and Cys-392 (C³⁹²) by a novel Caspase-like protease in the nucleus early in apoptotic process. The cleaved carboxy-terminal products are translocated to the cytoplasm early in apoptosis before chromatin condensation and nuclear fragmentation.
- Cleavage of Rad21 close to its endogenous, apoptotic cleavage site is sufficient to induce apoptosis in both apoptosis sensitive and resistant cells providing a direct and novel role of Rad21 in apoptosis.
- Overexpression of the 60 and 64 kDa cleavage product results in apoptosis in MCF-7 breast cancer cells. Given the role of hRad21 in chromosome cohesion, the cleaved C-terminal product and its translocation to the cytoplasm may act as a nuclear signal for apoptosis.
- Studies show that Rad21 can be cleaved in Caspase-3 deficient MCF7 cells in which Caspase-7 activity is blocked by siRNA/antibody treatment suggest that Caspase-3 and -7 are not the essential proteases that cleave Rad21. Since Rad21 is a nuclear protein and the cleavage initially occurs in the nucleus, the protease that cleaves Rad21 may reside inside the nucleus. Caspase-2 is localized in nucleus, but it cannot cleave Rad21 *in vitro*. These findings suggest the presence of a novel Caspase or Caspase-like molecule in the nucleus that cleaves Rad21 early in apoptosis.
- hRad21 is overexpressed in human breast tumors and in a number of breast cancer derived cell lines in comparison to normal breast epithelial cells. There appears to be a positive correlation between tumor ploidy and expression of Rad21 in the adjacent normal tissues.

Reportable Outcomes

Manuscript:

Pati, D*, Zhang, N., and Plon, S.E. (2002). Linking sister chromatid cohesion to apoptosis: role of Rad21. *Molecular and Cellular Biology* 22: 8267-8277. (* **Corresponding author**).

Manuscript in Revision:

Zhang, N, Li, K, and **Pati, D**. A new model for sister chromatid cohesion in mammalian cells.

Manuscripts in Preparation:

Zhang, N., Allred, D.C. and **Pati, D**. Amplification of Rad21 in human breast cancer.

Pati, D. Role of chromosomal segregation proteins in apoptosis: Identification of a novel pathway.

Employment:

Four summer studentships were granted to Ulysses Burley (2002), Jessica S. Ross (2003), Alexander Rancier (2004), and Sidney Adeleke (2005) undergraduate students of Morehouse College, Fayetteville State University, Houston-Tillotson College, and Houston Baptist University respectively by the SMART program of Baylor College of Medicine to work on this project. SMART program is funded by the National Institute of Health, National Institute of General Medical sciences.

Funding:

Based on the results obtained from these studies I was successful in securing following grants:

1) R01 HL 00000-13 (Pati) 12/1/2005 – 11/30/2010

NIH/NCI Priority score 166 (percentile 8.8)

Mitotic regulation of apoptosis in leukemia

2) 2005 Cancer Center Pilot Project Award (Pati) 7/1/2005 – 6/30/2007

Chromosomal Cohesin Protein Rad21 as a Novel Therapeutic Target for Breast Cancer

Conclusion

In summary, in contrast to previously described functions of Rad21, in chromosome segregation and DNA repair, cleavage of the cohesion protein and translocation of the C-terminal cleavage products to the cytoplasm are early events in the apoptotic pathway that amplify the apoptotic signal in a positive feed back manner by activating more Caspases. It is apparent that cohesin Rad21 may act as an interface between cohesion and cell death, and its cleavage may signal subsequent events of apoptosis. These results provide the framework for establishing a link between sister chromatid cohesion and the apoptotic response that have not previously been tested in any model system. Furthermore, our studies indicate overexpression of Rad21 protein in human breast tumor specimens. Future studies will identify the physiological protease that cleaves Rad21 and role of hRad21 in the apoptotic response in normal and malignant cells.

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Appendix-I
Statement of Work
(Work accomplished)

Technical Objective 1:

Month	Task	Status
1-4	Assessment of hRad21 cleavage and its immunolocalization in breast cancer cells after induction of apoptosis with DNA-damaging, non-DNA-damaging agents and microtubule-damaging drugs. Construction of mutant hRad21 expression constructs	Completed

Technical Objective 1A:

5-9	Development of a <i>in vitro</i> cleavage assay for hRad21 and <i>in vivo</i> assay for Caspase activity and Caspase inhibitor studies	Completed
6-10	Mapping of the Rad21 cleavage site	Completed

Technical Objective 1B:

9-12	Construction of pTAT-hRad21 and pTAT-cleaved hRad21 expression plasmids. Expression and isolation of recombinant Tat-Rad21 fusion protein	Completed
13-18	Tansduction of TAT-hRad21 into mammary cells Cell cycle analysis, aneuploidy status and apoptosis assay of transduced cells	Completed

Technical Objective 1C:

Will not be carried out. A study published recently from another lab has performed similar experiments proposed in this objective. In this study by Chen et al. (2002) have examined the role of survivin on Rad21-induced apoptosis. These studies indicated that Rad21-induced apoptosis can be inhibited by anti-apoptotic proteins such as Survivin.

Technical Objective 2A & 2B:

Month	Task	Status
10-16	Southern blot analysis of <i>hRAD21</i> gene in breast cancer cell lines	Completed
12-36	LOH and mutational studies	Abandoned.

Technical Objective 2C & 2D:

Month	Task	Status
1-4	Isolation of RNA, DNA and protein from breast tumor samples	Completed
5-12	Immunohistochemical localization and detection of Rad21 in human breast tumor sections	Completed
8-18	Northern and Western analysis of hRad21 transcripts and protein	Completed

expression in breast tumor specimens.

- 12-24 detection of apoptosis and aneuploidy in relation to Rad21 expression in breast tumor specimens
Abandoned due to technical difficulties.
- 32-36 Preparation of annual reports and manuscripts. . **Completed.**

Appendix-II
Bibliography of all publications and Meeting Abstracts

Journal Article:

Pati, D*, Zhang, N., and Plon, S.E. (2002). Linking sister chromatid cohesion to apoptosis: role of Rad21.
Molecular and Cellular Biology **22**: 8267-8277. (* **Corresponding author**).

Meeting Abstract:

Pati, D., and Plon, S.E. (2002). Linking sister chromatid cohesion to apoptosis: role of hRad21. Abstract book of the Cell Cycle meeting, Cold Spring Harbor Laboratory, New York, May15-19, 2002, p153.

Appendix-III
List of Personnel

Debananda Pati, Ph.D.	PI
Nenggang Zhang, Ph.D.	Postdoctoral Fellow
Gouqing Ge, BS	Technician

Appendix-IV (Published Manuscript)

Linking Sister Chromatid Cohesion and Apoptosis: Role of Rad21

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Rad21 is one of the major cohesin subunits that holds sister chromatids together until anaphase, when proteolytic cleavage by separase, a caspase-like enzyme, allows chromosomal separation. We show that cleavage of human Rad21 (hRad21) also occurs during apoptosis induced by diverse stimuli. Induction of apoptosis in multiple human cell lines results in the early (4 h after insult) generation of 64- and 60-kDa carboxy-terminal hRad21 cleavage products. We biochemically mapped an apoptotic cleavage site at residue Asp-279 (D²⁷⁹) of hRad21. This apoptotic cleavage site is distinct from previously described mitotic cleavage sites. hRad21 is a nuclear protein; however, the cleaved 64-kDa carboxy-terminal product is translocated to the cytoplasm early in apoptosis before chromatin condensation and nuclear fragmentation. Overexpression of the 64-kDa cleavage product results in apoptosis in Molt4, MCF-7, and 293T cells, as determined by TUNEL (terminal deoxynucleotidyltransferase-mediated dUTP-biotin nick end labeling) and Annexin V staining, assaying of caspase-3 activity, and examination of nuclear morphology. Given the role of hRad21 in chromosome cohesion, the cleaved C-terminal product and its translocation to the cytoplasm may act as a nuclear signal for apoptosis. In summary, we show that cleavage of a cohesion protein and translocation of the C-terminal cleavage product to the cytoplasm are early events in the apoptotic pathway and cause amplification of the cell death signal in a positive-feedback manner.

Normal development and homeostasis require the orderly regulation of both cell proliferation and cell survival. Cell cycle progression and control of apoptosis are thought to be intimately linked processes. Activation of the cell cycle plays a significant role in the regulation of apoptosis (16); in some cell types and under certain conditions, apoptosis has been shown to occur only at specific stages of the cell cycle (24). Mitosis and apoptosis are also closely interrelated (25), and the mitotic index is the most important determinant of the apoptotic index (25). Although proteins that regulate apoptosis have been implicated in the restraint of cell cycle entry (14) and the control of ploidy (29), the effector molecules at the interface between cell proliferation and cell survival have remained elusive.

Studies with yeast and higher eukaryotes, including humans, have indicated that an evolutionarily conserved protein complex, called cohesin, and its subunit, Mcd1/Sccl/hRad21, are required for appropriate arrangement of chromosomes during normal cell division (11, 28; for a review, see references 20, 30, 31, and 36). Analyses of Rad21 function in fission yeast, *Schizosaccharomyces pombe*, and of Sccl/Mcd1 function in budding yeast, *Saccharomyces cerevisiae*, have demonstrated that the nuclear phosphoprotein is required for appropriate chromosomal cohesion during the mitotic cell cycle and double-strand-break repair after DNA damage (1, 30). Biochemical analysis of cohesin indicates that it acts as a molecular glue, and human cohesin can promote intermolecular DNA catenation, a mechanism that links two sister chromatids together (26). In budding yeast, loss of cohesion at the metaphase-anaphase transition is accompanied by proteolytic cleavage of the Sccl/Mcd1 protein (11, 28, 30, 37) followed by its dissociation from the

chromatids (28, 30). Cleavage depends on a CD clan endopeptidase, Esp1 (also known as separin/separase) (37, 38), which is complexed with its inhibitor, Pds1 (securin), before anaphase (23, 39). In metaphase, ubiquitin-mediated degradation of the securin protein by APC/C-Cdc20 ubiquitin-ligase releases separin protein, which proteolytically cleaves cohesin Rad21, thereby releasing the sister chromatids (6, 7, 10, 18, 42). In budding yeast, fission yeast, and human cells, Rad21 has two mitotic cleavage sites for separase (12, 37, 38), and cleavage by separase appears to be essential for sister chromatid separation and for the completion of cytokinesis (12). In contrast to the simultaneous release of cohesin from the chromosome arms and centromere region in budding yeast by separase cleavage, most cohesin in metazoans is removed in early prophase from chromosome arms by a cleavage-independent mechanism (12, 39, 40). Only residual amounts of cohesin are cleaved at the onset of anaphase, coinciding with its disappearance from centromeres. Thus, Sccl/Mcd1/Rad21 plays a critical role in the eukaryotic cell division cycle by regulating sister chromatid cohesion and separation at the metaphase-to-anaphase transition.

Our results indicate that in addition to establishing and maintaining sister chromatid cohesion during mitosis, hRad21 plays a role in apoptosis, and its cleavage during apoptosis may act as a nuclear signal to initiate cytoplasmic events involved in the apoptotic pathway.

MATERIALS AND METHODS

Plasmids. Full-length *hRAD21* cDNA plasmid (K1AA 0078) in pBluescript SK(+) vector was obtained from Kazusa DNA Research Institute, Chiba, Japan. Full-length *hRAD21* cDNA was subcloned into several mammalian expression plasmids, including pFLAGCMV2, pCS2MT, and pCDNA6Myc-HisC, to produce epitope-tagged proteins where applicable. *hRad21* cDNA was also subcloned in frame upstream of the *myc* epitope in pCMV/*myc*/Nuc and pCMV/*myc*/Cyto (Invitrogen, Carlsbad, Calif.) to direct the expression of hRad21 protein to the nucleus and cytoplasm, respectively. The following plasmids were

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used for transfection: pCS2MT-*hRAD21* was constructed by in-frame ligation of the 2,331-bp *NcoI/DraI* fragment bearing the *hRAD21* cDNA to the end of the sixth *myc* epitope in pCS2MT (B. Kelley, Fred Hutchinson Cancer Center, Seattle, Wash.); pFLAGCMV2-*hRAD21* was generated by cloning the full-length *hRAD21* gene contained on a 2,578-bp *MscI/StuI* fragment from pSKKIAA0078 into pFLAGCMV2 (Kodak) that was digested with *SmaI*.

Site-directed mutagenesis of *hRad21*. pCS2MT-*hRAD21* apoptotic cleavage site (ACS) mutants I (PDSPD²⁷⁹S to PDSPA²⁷⁹S) and II (PD²⁷⁶S²⁷⁷PD²⁷⁹S²⁸⁰ to PA²⁷⁶A²⁷⁷PA²⁷⁹A²⁸⁰) were generated using a PCR-based site-directed mutagenesis protocol as previously described (33). The PCR resulted in a 550-bp internal *hRAD21* fragment containing the mutations. A 221-bp piece of wild-type (WT) *hRAD21* (from the *BsgI* to *PFLFI* sites) was replaced with the comparable mutated fragment. The resulting plasmids, pCS2MT-*hRAD21*-ACS-mut-I and pCS2MT-*hRAD21*-ACS-mut-II, were verified by DNA sequencing. The amino-terminal (N-*hRad21*, encoding amino acids [aa] 1 to 279) and carboxy-terminal (C-*hRad21*, encoding aa 280 to 631) cleavage products were cloned into *myc* epitope-tagged pCS2MT vectors by using PCR amplification of the fragments from the *hRAD21* cDNA. These constructs were also verified by DNA sequencing.

Generation of *hRad21* pAb and mAb. Rabbit polyclonal antibody (pAb) was raised commercially (Covance, Denver, Pa.) against synthetic peptides corresponding to the sequence of the 14 carboxy terminal aa of *hRad21* (SDIIAT-PGPRFHII). Immunization and affinity purification of antibodies were performed according to the manufacturer's protocol. Monoclonal antibody (mAb) against a partial recombinant *hRad21* protein (aa 240 to 631) was also raised commercially (Imgenex, San Diego, Calif.). Both antibodies had very high titers, as determined by enzyme-linked immunosorbent assay. Both antibodies recognized the WT *hRad21* protein as a specific 122-kDa band in Western blot analysis and effectively immunoprecipitated endogenous *hRad21* from various human and rodent cell lines and tissue lysates. Immunodetection of the 122-kDa band was blocked competitively by pretreatment of the lysates with recombinant *hRad21* protein or synthetic C-terminal peptides. Both antibodies were also effective in immunohistochemistry and immunofluorescence staining of both paraffin-embedded and tissue culture slides.

Antisera. The monoclonal antisera were obtained as follows: human poly-(ADP-ribose) polymerase (PARP) from PharMingen, San Diego, Calif.; Flag epitope and mouse β -actin from Sigma, St. Louis, Mo.; c-*myc* epitope (9E10), bacterial *tpfE*, caspase-3, caspase-7, tubulin, and lamin from Oncogene Research Products, Cambridge, Mass. *hRad21* N-terminal antibody was a gift from J.-M. Peters (Research Institute of Molecular Pathology, Vienna, Austria).

Cell cultures and transfection. MCF-7 breast carcinoma cells, human choriocarcinoma JEG3 cells, and IMR90 primary lung fibroblast cells were obtained from the American Type Culture Collection (ATCC) and were maintained per ATCC protocol. Human Molt4 and Jurkat T-cell leukemia cells (both obtained from ATCC) were grown in RPMI 1640 medium supplemented with 10% fetal bovine serum and maintained at 37°C, 95% humidity, and an atmosphere of 5% CO₂. EL-12 mouse mammary epithelial cells were obtained from the Medina Laboratory (Baylor College of Medicine) and maintained as previously described (27). Cells were transfected with appropriate plasmids in 100-mm-diameter dishes using Superfect or Effectene reagents from Qiagen (Valencia, Calif.) according to the manufacturer's protocol. A fixed amount of plasmid DNA was used in any given experiment. The total amount of expression vector DNA was equalized by the addition of blank vectors to control for promoter competition effects. When necessary, transfection efficiency was monitored by use of 1 μ g of pDsRedi-Mito plasmid (Clontech, Palo Alto, Calif.) per transfection. Transfection efficiency was determined by counting the percentage of red fluorescent cells in five random fields under a microscope with appropriate fluorescent channels.

Drug treatments. Etoposide (VP-16) (20-mg/ml injections) and camptothecin were purchased from GensiaSicor Pharmaceuticals (Irvine, Calif.) and Sigma, respectively. Camptothecin was dissolved in dimethyl sulfoxide (DMSO) and stored in aliquots at -20°C. Cells were plated at a concentration of 6×10^6 cells/ml and treated with appropriate concentrations of drugs. Molt4 cells were treated with etoposide, while Jurkat cells were treated with camptothecin for 8 h unless otherwise indicated. Controls were treated with equivalent dosages of vehicle. The caspase inhibitor z-VAD-FMK was also dissolved in DMSO and stored at -20°C. Peptide aldehydes MG115 and MG132 were obtained from Peptide Institute, Inc. (Lexington, Ky.) and dissolved at a concentration of 10 mM in DMSO. Cells were treated with a 0.025 mM concentration of proteasome inhibitors for 8 h before harvesting. 15-Deoxy-delta(12,14)-prostaglandin J₂ (15dPGJ₂) was purchased from Cayman Chemical Co. (Ann Arbor, Mich.). Induction of apoptosis in JEG3 cells by using 15dPGJ₂ was carried out as previously described (19).

Protein analysis and IP. Cells were pelleted by low-speed centrifugations (800 \times g for 5 min) and lysed in RIPA buffer (phosphate-buffered saline [PBS], 1% Nonidet P-40, 0.1% sodium dodecyl sulfate [SDS], 0.5% sodium deoxycholate) or PBSTDS buffer (PBS, 1% Triton X-100, 0.1% SDS, 0.5% sodium deoxycholate) containing protease and phosphatase inhibitors (1 mM EDTA, 0.2 mM phenylmethylsulfonyl fluoride, 1 μ g of pepstatin per ml, 30 μ l of aprotinin per ml, 0.5 μ g of leupeptin per ml, 100 mM sodium orthovanadate, 100 mM sodium fluoride) (all from Sigma) for 10 to 15 min on ice, followed by passage through a 21-gauge needle. When appropriate, additional phosphatase inhibitor cocktails I and II (Sigma) were added to the lysis buffer at a dilution of 1:100. Lysates were then centrifuged at 1,000 \times g for 20 min, and the supernatants were aliquoted and frozen at -80°C until use. Protein samples were also made from the cytoplasmic and nuclear fractions of apoptosis-induced Molt4 cells by using protocols previously described (5). The purities of the cytosolic and nuclear fractions were verified by Western blotting with antibodies to tubulin and nuclear lamin, respectively. After protein quantification (using detergent-compatible protein dye and bovine serum albumin from Bio-Rad as standards) and normalization, 10 to 40 μ g of protein extracts was electrophoresed on SDS-polyacrylamide gel electrophoresis (PAGE) gels and transferred to polyvinylidene difluoride (PVDF) membranes (Millipore, Bedford, Mass.). The filters were initially blocked with 5% nonfat dry milk in Tris-buffered saline containing 0.1% Tween 20 for 1 to 2 h at room temperature and then probed with *hRad21* mAb or *hRad21* pAb at a 1:1,000 dilution, 1.5 μ g of *myc* epitope/ml, 2.5 μ g of Flag epitope/ml, β -actin at a 1:100,000 dilution, or PARP antiserum at a 1:2,000 dilution. The bound antibodies were visualized by the enhanced chemiluminescence detection system (Amersham, Buckinghamshire, England), in combination with the horseradish peroxidase-conjugated anti-mouse or anti-rabbit secondary antibodies as appropriate, and the intensity of the specific bands in the exposed films was quantified. In some of the later experiments, bound primary antibodies were detected with IRD800 dye-labeled, appropriate species-specific secondary antisera and the signal was visualized on a Li-Cor (Lincoln, Neb.) Odyssey infrared scanner. Immunoprecipitation (IP) was performed as follows. A 1.0-ml sample of cell lysate was precleared by incubation with 10 μ l of normal mouse immunoglobulin G (IgG) and 20 μ l of protein G plus agarose (Oncogene Research Products) at 4°C for 1 h on a rotator. The precleared lysate was collected after centrifugation at 800 \times g for 15 min. A 0.5- to 1.0-ml sample of precleared lysate normalized for protein concentrations was incubated at 4°C for 1 h with primary antibodies followed by the addition of 20 μ l of protein A and protein G plus agarose. The mix was then incubated at 4°C for another 12 to 16 h on a rotator. Precipitates were then washed four times with 1 ml of ice-cold PBS, with a final wash in the lysis buffer before electrophoresis and Western blot analysis.

Mapping of *hRad21* apoptotic cleavage sites. Apoptosis was induced in Molt4 T cells by treatment with 10 μ M etoposide for 8 h. Protein lysates were subjected to IP using *hRad21* mAb or a control bacterial *tpfE* mAb. The immunoprecipitated samples were run on SDS-6% PAGE gels that included 0.1 mM sodium thioglycolate (Sigma) as a scavenger in the upper running buffer. Electrophoresed samples were then electroblotted onto PVDF membranes at 400 mA for 45 min at room temperature (~25°C) using CAPS [3-(cyclohexylamino)propane-sulfonic acid] buffer (10 mM CAPS, 10% methanol, pH 11). At the end of the transfer, the blotted membranes were rinsed with water for 2 to 5 min, stained with 0.05% Coomassie blue in 1% acetic acid-50% methanol for 5 to 7 min, destained in 50% methanol until the background was pale blue (5 to 15 min), and finally rinsed with water for 5 to 10 min. Appropriate bands were cut out and air dried and sent to the protein chemistry core laboratory at Baylor College of Medicine for N-terminal sequencing.

Immunocytochemistry and detection of apoptosis. EL-12 cells were grown on Falcon culture slides. Medium was poured off before the cells were treated with UV (0, 50, 100, or 200 J/m²). Fresh medium was added immediately after UV radiation. Cells were fixed with cold methanol after 6 h of UV treatment unless otherwise noted. Double staining of *hRad21* was performed by incubating anti-*hRad21* mAb and rabbit anti-C-terminal-*hRad21* pAb. The signals of mAb and pAb were visualized by the addition of rhodamine-labeled goat anti-mouse IgG (1:100) and fluorescein-labeled goat anti-rabbit IgG (1:800) (Molecular Probes), respectively. Slides were mounted with Vectashield mounting medium with DAPI (4',6'-diamidino-2-phenylindole; H-1200, Vector) and sealed with nail makeup. Images were obtained with a Zeiss inverted fluorescence microscope coupled to an Axiocam high-resolution digital camera operated with Axiovision 3.0 software (Carl Zeiss Inc., Thornwood, N.Y.).

For detection of apoptosis in transiently transfected 293T and MCF-7 cells, 1 million cells were seeded onto 100-mm-diameter culture dishes 2 days prior to transfection. Cells were transfected with the indicated *hRad21* constructs when they reached 60% confluence. For DAPI staining, cells were cotransfected with 5 μ g of pDsRedi-Mito (Clontech) and 5 μ g of pCS2MT, pCS2MT *Rad21* wild

type, pCS2MT Rad21 N terminus, or pCS2MT Rad21 C terminus by using the calcium phosphate method. At 16, 24, and 48 h posttransfection, cells were detached with trypsin and collected by centrifugation at $1,000 \times g$ for 5 min. The samples were fixed with 4% paraformaldehyde in PBS (pH 7.2), mounted with Vectashield mounting medium with DAPI (H-1200, Vector), and examined by fluorescence microscopy. The intact and degraded nuclei of cells coexpressing pDsRed1 (with red fluorescence) were counted. About 50 fluorescent nuclei from each treatment group were screened and counted for normal morphology (rounded chromatin) or for apoptotic nuclei (fragmented and condensed chromatin). Data were expressed as the percentage of apoptotic cells among total counted cells. Each treatment was replicated three times. For Annexin V and TUNEL (terminal deoxynucleotidyltransferase-mediated dUTP-biotin nick end labeling) staining, 293T cells were transfected with 10 μ g of pCS2MT, pCS2MT Rad21 wild type, pCS2MT Rad21 N-terminus, or pCS2MT Rad21 C-terminus by using the calcium phosphate method. After 16, 24, and 48 h, the cells were detached and collected as described above. Annexin V (Annexin V-FITC [fluorescein isothiocyanate] apoptosis direction kit) and TUNEL staining (MBE-STAIN apoptosis kit direct) were performed according to the manufacturer's protocol (MBL, Watertown, Mass.). Staining of the cells with Annexin V-FITC and propidium iodide (PI) was used to distinguish between cells undergoing apoptosis (PI negative) and those that were necrotic or dead (PI positive). Apoptotic cells were identified with TUNEL staining using fluorescein-dUTP as the substrate.

The caspase-3 activities in Molt4 cells were measured using a caspase-3 assay kit from Clontech according to the manufacturer's protocol.

Proteolytic cleavage assay of the in vitro transcribed and translated hRad21.

35 S-hRad21 or unlabeled (nonisotopic) hRad21 was produced by in vitro transcription-translation using the TNT rabbit reticulocyte lysate system (Promega, Madison, Wis.). Rabbit reticulocyte lysate was combined with 1 μ g of plasmid DNA containing either the WT *hRAD21* cDNA (pCS2MT-*hRAD21*) or one of the *hRAD21* ACS mutants, ACS-mut-I or ACS-mut-II, and SP6 RNA polymerase. Reaction in the absence of plasmid DNA served as a negative control. Reaction mixtures were incubated at 30°C for 90 min. In vitro cleavage reaction was performed as previously described (9). In brief, 6 μ l of in vitro translated 35 S-hRad21 (WT), ACS-mut-I, or ACS-mut-II was combined with 30 μ l of reaction buffer (20 mM HEPES, pH 7.4, 2 mM dithiothreitol, 10% glycerol) and one of the following enzyme sources: 2 μ l (200 U) of recombinant caspase-3, 2 μ l (4 U) of caspase-7, or 2 μ l (10 μ g) of Molt4 cell lysates (treated with DMSO or 10 μ M etoposide for 6 h). The cleavage reaction was performed at 37°C for 1 h, after which 8 μ l of 6 \times sample buffer with dithiothreitol was added to stop the reaction. Twenty microliters of this reaction was electrophoresed on SDS-6% PAGE gels, fixed with methanol and acetic acid for 30 min, dried on a gel dryer, and exposed to a Storm imager. Bands were quantified using ImageQuant 5.2 software (Molecular Dynamics, Inc., Sunnyvale, Calif.). Unlabeled (nonisotopic) hRad21 from the TNT reactions was also incubated as described above in the presence or absence of caspase-3 or caspase-7. Samples were then analyzed by SDS-PAGE followed by Western blotting with hRad21 antiserum.

Data analysis. The differences between the apoptosis levels in cells transfected with various hRad21 constructs were measured using a paired test of proportions based on binomials (8). The results of the caspase-3 activity assay were analyzed using Student's *t* test.

RESULTS

We report the role of hRad21 in the apoptotic response and cleavage of hRad21 protein in human cells by a caspase-like activity.

Cleavage of hRad21 during apoptosis. While examining the expression of Rad21 in mammalian cells after DNA damage, we surprisingly identified the cleavage of hRad21 protein after induction of apoptosis. hRad21 was cleaved during etoposide-induced apoptosis in human Molt4 T-cell leukemia cells. Induction of apoptosis resulted in the generation of approximately 64- and 60-kDa cleavage products, as determined with an hRad21 mAb (Fig. 1). The cleavage of hRad21 in Molt4 cells was a function of etoposide dosage (Fig. 1A), as the ratio of cleaved hRad21 to full-length protein appeared to be directly proportional to increasing doses of etoposide over the tested range (10 to 50 μ M). hRad21 cleavage products were

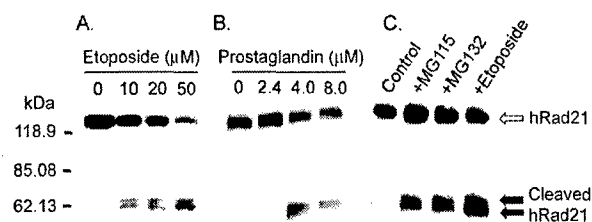


FIG. 1. Apoptosis-induced cleavage of hRad21 in Molt4 T-cell leukemia and JEG3 choriocarcinoma cells treated with etoposide, prostaglandin, and proteasome inhibitors. (A) Dose-related cleavage of hRad21 in Molt4 T-cell leukemia cells treated with increasing concentrations of etoposide (10 to 50 μ M) for 6 h. (B) JEG3 cells treated with 15DPGJ₂ (2.4 to 8 μ M) for 16 h. (C) Molt4 cells were also treated with a 0.025 mM concentration of proteasome inhibitors, MG115, and MG132 for 8 h. Lysates of these samples were resolved on an SDS-PAGE (4 to 20% acrylamide) gel, transferred to a nitrocellulose membrane, and analyzed by Western blot using a monoclonal hRad21 antibody. Induction of apoptosis resulted in the generation of approximately 64- and 60-kDa hRad21 cleavage products (shown by the closed arrows). Full-length hRad21 (122 kDa) is indicated by the open arrow.

also detected in a number of other cell lines following induction of apoptosis by DNA-damaging agents (ionizing radiation and topoisomerase inhibitors) (data not shown) and/or non-DNA-damaging agents (prostaglandin [Fig. 1B], proteasome inhibitor [Fig. 1C], cycloheximide treatment, and cytokine withdrawal [data not shown]). In addition, equivalent doses of ionizing radiation in cells that are resistant to apoptosis (Raji lymphoid leukemia and H1299 large-cell lung carcinoma cells) did not generate this band (data not shown); thus, it was not a simple by-product of DNA damage.

Translocation of the carboxy-terminal hRad21 fragment to the cytoplasm after induction of apoptosis. Molt4 cells were treated with 10 μ M etoposide for 0, 1, 2, 3, 4, 6, and 12 h. Induction of apoptosis was verified by determination of caspase-3 activity (Fig. 2A), Annexin V staining (Fig. 2F), the cleavage of PARP, and the morphology of DAPI-stained nuclei (data not shown). Western blot analysis of cytoplasmic and nuclear fractions by using a C-terminal hRad21 antibody detected a 122-kDa protein band in the noninduced cells (0 h), and as reported before (12), full-length hRad21 was found exclusively in the nuclear fractions (Fig. 2B). However, induction of apoptosis resulted in the early (4 h after induction) generation of approximately 64- and 60-kDa cleavage products, as determined by a C-terminal hRad21 antibody (Fig. 2B). As indicated by Annexin V staining, hRad21 cleavage shows a clear temporal relationship with the early events of apoptosis when the cell membrane remains intact. Annexin V is a calcium-dependent, phospholipid binding protein with high affinity for phosphatidylserine (PS) and can be used to identify apoptotic cells with exposed PS. As PS exists in the inner face of the cell membrane in normal cells, Annexin V cannot bind to the cell membrane. Early in apoptosis, however, PS is translocated from the inner to the outer surface of the cell membrane. As Annexin V has high affinity for PS, it can then bind to the cell surface via interaction with PS. In the late stages of apoptosis, Annexin V continues to bind PS, and as the membrane permeability is increased, PI can enter the cell and bind DNA. In addition to our results with Annexin V staining,

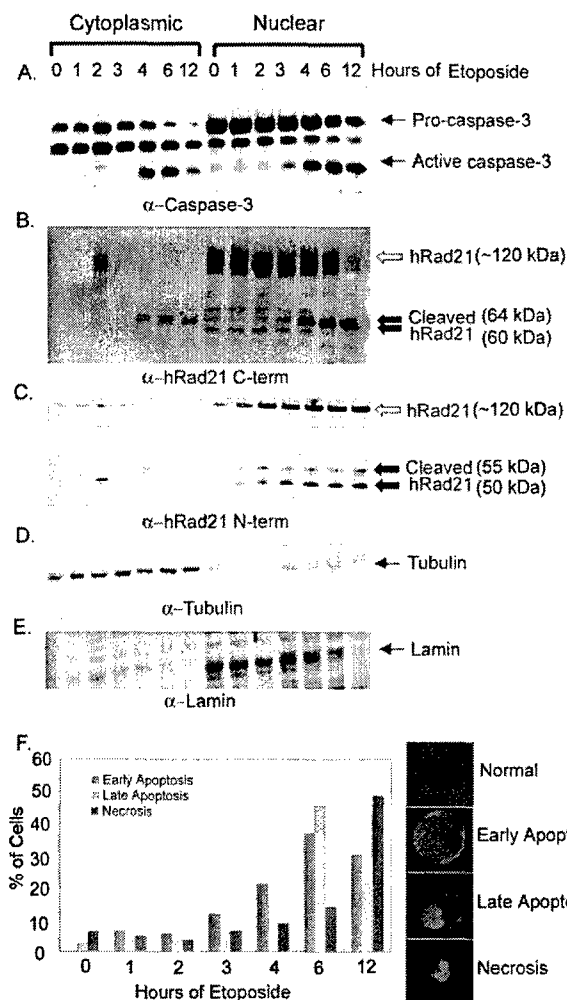


FIG. 2. Time course of etoposide-induced hRad21 cleavage. Molt4 cells were incubated in the absence (0 h) or presence of 10 μ M etoposide for 1, 2, 3, 4, 6, and 12 h. At the end of the incubation period, lysates from cytoplasmic and nuclear fractions were made. (A) Induction of apoptosis was verified by determination of caspase-3 activity in a Western blot analysis using anti-caspase-3 mAb. Pro-caspase-3 and active caspase-3 are indicated. (B and C) The time course of cleavage of hRad21 protein in etoposide-induced cytoplasmic and nuclear fractions was examined using C-terminal (B) and N-terminal (C) Rad21 pAbs. Full-length hRad21 (122 kDa; open arrow) and C-terminal cleaved 60- and 64-kDa fragments (closed arrows) are indicated. (D and E) The purities of the cytoplasmic (D) and nuclear (E) fractions were verified with antibodies to tubulin and nuclear lamin, respectively. (F) Quantitative measurement of Annexin V staining showing early and late events of apoptosis. Cells stained with Annexin V (green fluorescence in the outer cell membrane) represent early stages of apoptosis, while cells with both PI-stained nuclei (red fluorescence) and Annexin V staining (green fluorescence in the outer cell membrane) represent late stages of apoptosis. Cells with PI-stained red fluorescence represent necrotic cells only. Normal cells lack any staining. Examples from each category are shown at right. Values represent the percentage of green (early stage of apoptosis), green plus red (late stage of apoptosis), or red (necrotic) fluorescent cells, with 120 cells being used at each time point.

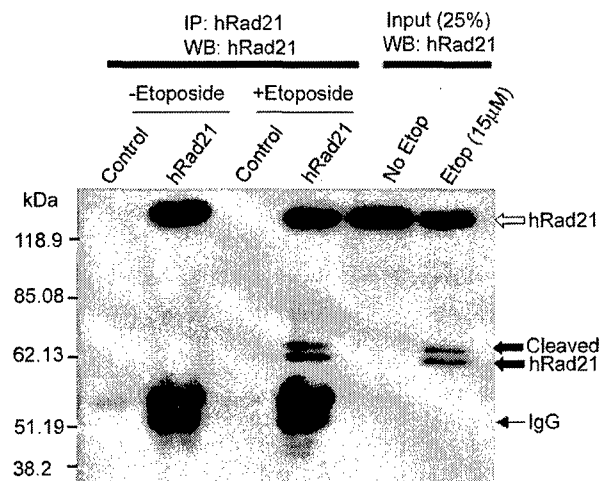


FIG. 3. IP and Western blot (WB) analyses of the hRad21 cleavage products. Apoptosis was induced in Molt4 T cells by treatment with 10 μ M etoposide (Etop) for 8 h. Protein lysates were subjected to IP using hRad21 mAb or a control bacterial *trpE* mAb. Both monoclonal and polyclonal C-terminal antibodies detected 64- and 60-kDa bands (closed arrows), indicating that these bands are from the C-terminal portion of the cleaved protein.

we found that the progressive increase in the cleavage of hRad21 correlates with the level of active caspase-3 (Fig. 2A).

Although hRad21 is a nuclear protein, the cleaved products are found in both nuclear and cytoplasmic fractions after induction of apoptosis (Fig. 2B). The identities of these two cleavage products were investigated using an N-terminal hRad21 antibody. As expected, the N-terminal antibody could not detect the 64- and 60-kDa cleavage products either in the cytoplasmic or nuclear fraction. In contrast, this antibody detected two other bands (approximately 50 and 55 kDa) only in the nuclear fractions (Fig. 2C). The purities of the cytosolic and nuclear fractions were verified with antibodies to tubulin and lamin, respectively (Fig. 2D and E). These results indicate that hRad21 may potentially be cleaved at two different sites following induction of apoptosis. The C-terminal hRad21 cleavage products but not the N-terminal hRad21 products are found in the cytoplasm after cleavage following induction of apoptosis.

The identities of the cleavage products were confirmed through recognition by mAbs to hRad21 in IP and Western blot analyses (Fig. 3). hRad21 mAb selectively immunoprecipitated both the 60- and 64-kDa hRad21 cleavage products, along with the native 122-kDa full-length hRad21 protein in etoposide-induced Molt4 cells. Analysis of cells treated with vehicle only and control IP with isotype bacterial TrpE antibody did not detect these bands, confirming that the cleaved bands were hRad21 products. Both monoclonal and polyclonal C-terminal antibodies detected the 64- and 60-kDa bands, confirming that these bands were derived from the C-terminal portion of the cleaved protein.

Translocation of hRad21 was further investigated in EL-12 mammary epithelial cells by immunofluorescence staining using the monoclonal and C-terminal hRad21 polyclonal antisera. Unlike Molt4 cells, EL-12 cells have a large cytoplasm to facilitate visualization. In these cells, Rad21 was entirely nu-

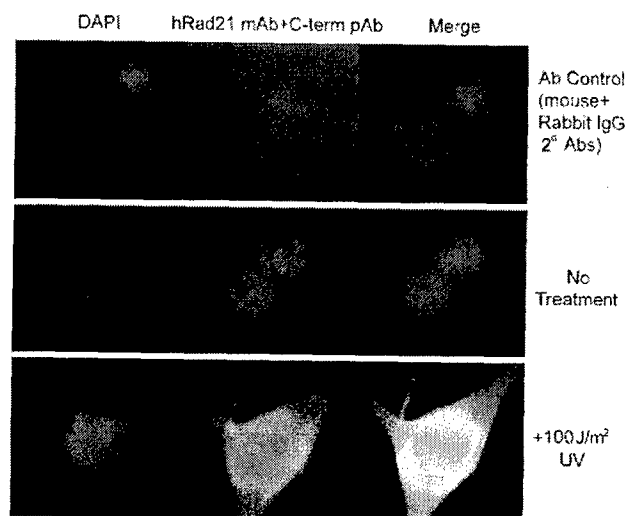


FIG. 4. C-terminal Rad21 cleavage product translocates to the cytoplasm after induction of apoptosis. Apoptosis was induced by treatment of EL-12 mammary epithelial cells with UV light (100 J/m^2). UV-treated (bottom panel) and untreated control (middle panel) cells were subjected to immunofluorescence staining and microscopy using a C-terminal hRad21 pAb (green fluorescence) and hRad21 mAb (red fluorescence), respectively. The signals of mAb and pAb were visualized by the addition of rhodamine-labeled goat anti-mouse IgG and fluorescein-labeled goat anti-rabbit IgG, respectively. The upper panel shows the background staining (negative control) from the fluorescein-labeled secondary antibody in the presence of normal mouse and rabbit IgGs. The nuclear material is visualized by DAPI staining (blue fluorescence). Panels at right show merged images of red, blue, and green fluorescence.

clear (Fig. 4, middle panel). Apoptosis was induced by treatment of EL-12 cells with UV light (100 J/m^2) and was verified by the cleavage of Rad21 and PARP (data not shown). Immunofluorescence staining of the UV-treated cells by the C-terminal antibody clearly demonstrated translocation of the cleaved C-terminal Rad21 to the cytoplasm (Fig. 4, bottom panel).

Inhibition of hRad21 cleavage by caspase peptide inhibitors. Peptide-based caspase inhibitors inhibited the apoptosis-induced cleavage of hRad21, suggesting the involvement of caspases in hRad21 cleavage (Fig. 5). Molt4 cells were treated with $20 \mu\text{M}$ z-VAD-FMK, a broad-spectrum caspase inhibitor, 1 h prior to etoposide ($10 \mu\text{M}$) treatment. As shown in Fig. 5, treatment with z-VAD-FMK completely blocked etoposide-induced hRad21 cleavage. In an *in vitro* cleavage assay (described below), z-VAD-FMK also inhibited caspase-3-induced cleavage of ^{35}S -hRad21 (data not shown).

Identification of the apoptotic cleavage site in hRad21. The hRad21 cleavage site was mapped through N-terminal sequencing of the immunoprecipitated hRad21 cleavage products from electroblotted and Coomassie-stained PVDF membranes (Fig. 6). Sequencing of the 64-kDa band revealed that hRad21 was cleaved at Asp-279 (D^{279}). The N-terminal sequence of the 64-kDa band was SVDPVEP. In the full-length protein, the sequence immediately N terminal to the D^{279} cleavage site was PDSPD 279 . Thus, there was a repeat of the PDS sequence encompassing the cleavage site, i.e., PDSPD 279 /SVDPVEP (Fig. 6A). We were not successful in sequencing

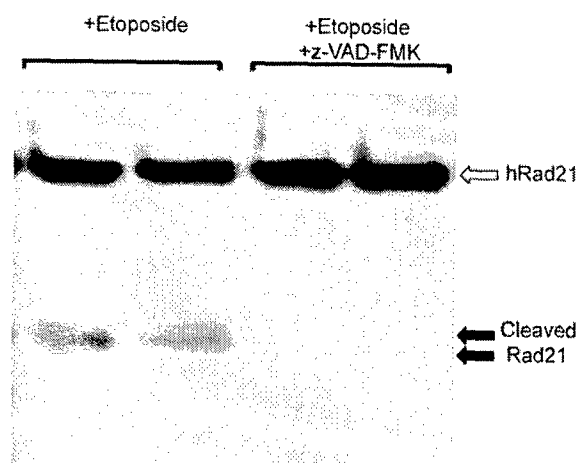


FIG. 5. Caspase peptide inhibitors inhibit etoposide-induced cleavage of hRad21. Molt4 cells were treated with $20 \mu\text{M}$ z-VAD-FMK, a broad-spectrum caspase inhibitor, 1 h prior to etoposide ($10 \mu\text{M}$) treatment for 6 h. At the end of the incubation period, protein lysates were analyzed on an SDS-6% PAGE gel followed by Western blot analysis using hRad21 C-terminal pAb.

the 60-kDa band, possibly because of an N-terminal blocking effect. To verify whether specific cleavage occurred at D^{279} in hRad21 after induction of apoptosis, we introduced a point mutation (mut-I) by substituting an alanine (A) for aspartate (D) at this position of hRad21 (D^{279}A) (Fig. 6B). Furthermore, because of the repetition of the cleavage sequence $^{275}\text{PDSPDS}^{280}$, we made a second mutant construct (mut-II) by substituting alanine (A) for both aspartate (D) and serine (S) residues, i.e., hRad21 ($^{275}\text{PDSPDS}^{280}$ to $^{275}\text{PAAPAA}^{280}$). We then transiently transfected Molt4 cells with WT or mutant hRad21 constructs tagged with the *myc* epitope at the N terminus and treated these cells with etoposide as indicated. As shown in Fig. 6C, antibody against *myc* tag (9E10) revealed the proteins encoded by the transfected hRad21 WT and hRad21 ACS-mut-I and ACS-mut-II constructs. However, the cleavage fragments were detected only for WT hRad21, not for either of the mutants, indicating that a point mutation at D^{279} prevented cleavage (Fig. 6C). We reprobed the blot with anti-hRad21 mAb and found that both the 60- and 64-kDa C-terminal fragments were present in all etoposide-treated cells (data not shown), confirming that endogenous hRad21 was cleaved in cells transfected with hRad21 mutants.

Involvement of caspases in hRad21 cleavage. Closer inspection of the adjoining sequence at the Rad21 apoptotic cleavage site (DSPD^{279}) (Fig. 6A) revealed a putative recognition sequence for a primitive caspase, Ced3. This sequence is conserved Rad21 in vertebrates, including humans, mice, and frogs (*Xenopus* spp.). The sequence of the putative cleavage site, together with the inhibitory effect of a panel of caspase inhibitors on etoposide-induced apoptosis in Molt4 cells, indicated the possible involvement of a caspase family protease. While the experiments with caspase inhibitors suggested the involvement of a caspase family of protease(s) in the pathway leading to hRad21 cleavage, they did not demonstrate direct internal cleavage of hRad21 by a caspase. We therefore utilized an *in vitro* cleavage assay as described previously for the retinoblas-

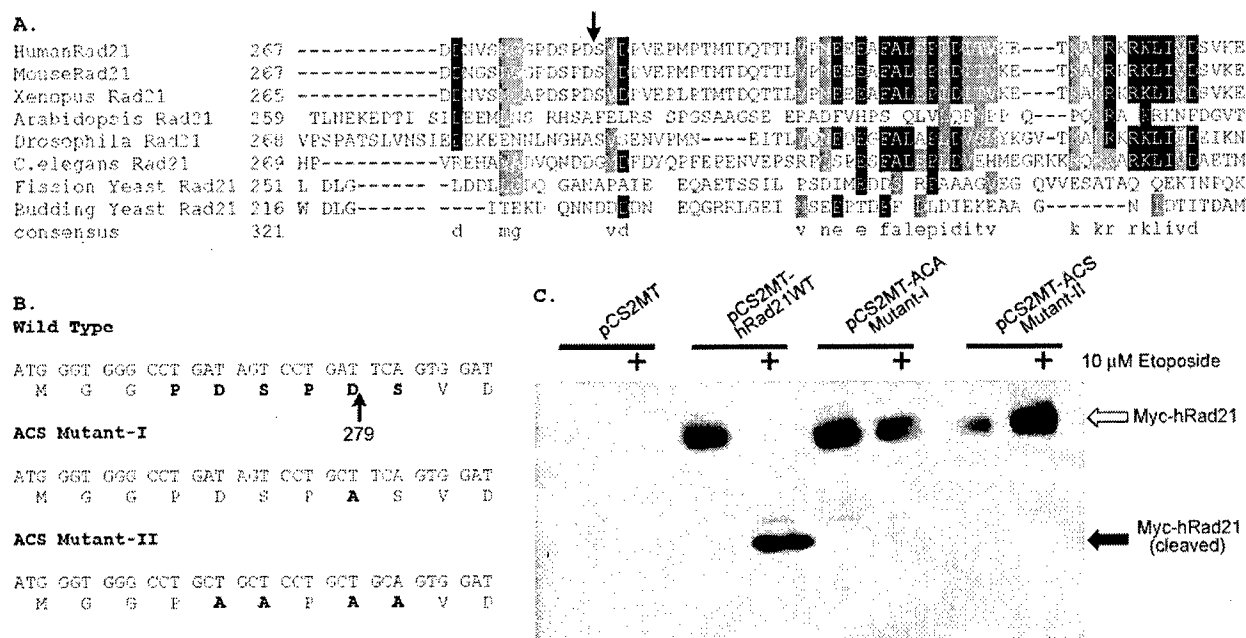


FIG. 6. Characterization of the apoptotic cleavage site of hRad21. The hRad21 cleavage site was mapped biochemically, as described in Materials and Methods, through N-terminal sequencing of a Coomassie-stained PVDF membrane that was electroblotted with immunoprecipitated hRad21 cleavage products. (A) Comparison of the apoptotic cleavage recognition site and the adjoining sequence of hRad21 with those of other vertebrates (MouseRad21 and Xenopus Rad21) and simpler eukaryotes. *C.elegans*, *Caenorhabditis elegans*. The arrow indicates the peptide bond cleaved during apoptosis. (B) Construction of the apoptotic cleavage site mutants, ACS-mut-I and ACS-mut-II, to verify whether specific cleavage occurs at D²⁷⁹ in hRad21 after induction of apoptosis, by introduction of a point mutation to substitute an alanine (A) for aspartate (D) (mut-I) or alanine (A) for aspartate (D) and serine (S) (mut-II). (C) Molt4 cells were transiently transfected with blank vector (pCS2MT), WT hRad21 (pCS2MT-hRad21), or ACS mutants tagged with myc epitope at their N termini (pCS2MT-ACSmut-I or pCS2MT-ACSmut-II) and treated with etoposide as indicated. Lysates were analyzed with SDS-6% PAGE followed by Western blot analysis using antibody against myc tag (9E10) to distinguish the cleavage products from the native forms of transfected hRad21 WT and hRad21 ACS-mut-I and ACS-mut-II proteins.

toma protein (9) to examine the ability of purified caspase to cleave hRad21 (Fig. 7). We used two caspases, caspase-3 and caspase-7, that are major regulators of apoptosis in diverse cell types (35) (Fig. 7A), along with lysates from Molt4 cells treated with etoposide (apoptotic lysate) or vehicle (nonapoptotic lysate), to examine their role in hRad21 cleavage (Fig. 7B). Together, caspase-3 and caspase-7 comprise the caspase-3 subfamily, and both enzymes recognize and cleave after the consensus cleavage site DXND (E. S. Alnemri, D. J. Livingston, D. W. Nicholson, G. Salvesen, N. A. Thornberry, W. W. Wong, and J. Yuan, Letter, Cell 87:171, 1996). Addition of recombinant caspase-3 or caspase-7 to the in vitro transcribed and translated hRad21 in rabbit reticulocyte lysates clearly resulted in the production of a 64-kDa hRad21 fragment (Fig. 7A and B). The 64-kDa fragment produced by these caspases precisely comigrated with the 64-kDa band produced by apoptotic Molt4 lysates, while the control (nonapoptotic) cell lysate could not cleave hRad21 protein. On the other hand, both of the hRad21 ACS mutants failed to be cleaved by these two caspases or by apoptotic cell lysates in this assay, strongly suggesting that caspase-3- or caspase-7-like enzymes in the apoptotic cells or extracts were responsible for cleavage at the putative caspase recognition site (D²⁷⁹) of hRad21.

In addition to the 64-kDa fragment, several other fragments were generated by caspase-3 and -7. It is possible that the 64-kDa fragment was degraded further by these caspases, re-

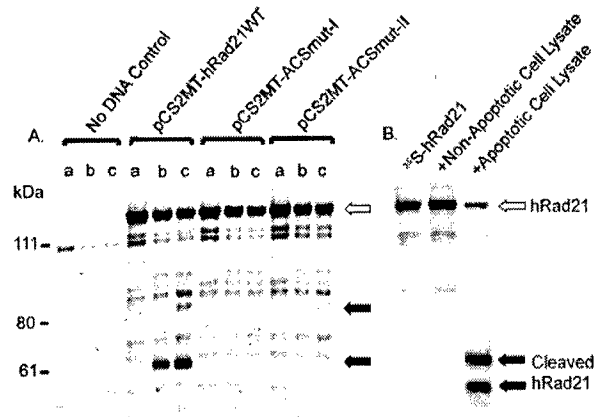


FIG. 7. Cleavage of in vitro translated hRad21 by recombinant caspase-3 and caspase-7. (A) In a cleavage reaction, in vitro translated unlabeled (nonisotopic) WT hRad21 or ACS mutant hRad21 (ACS-mut-I or ACS-mut-II) in the rabbit reticulocyte lysate were incubated with saline (vehicle) (lanes a), caspase-3 (lanes b), or caspase-7 (lanes c). TNT reactions in the absence of plasmid DNA served as a negative control. Samples were analyzed on an SDS-6% PAGE gel followed by Western blotting with hRad21 C-terminal pAb. Molecular weight markers are shown at left. (B) ³⁵S-hRad21 was incubated in the absence of extract (left lane) or in the presence of Molt4 cell lysates treated with DMSO (middle lane) or 10 μ M etoposide (right lane) for 6 h. Samples were resolved on a 4 to 20% gradient SDS-PAGE gel, fixed with methanol and acetic acid for 30 min, dried on a gel dryer, and exposed to a Storm imager.

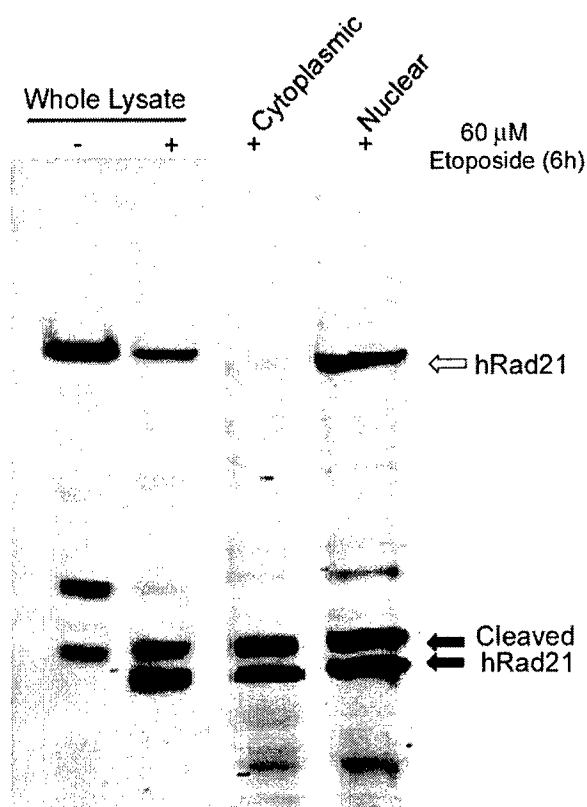


FIG. 8. Cleavage of hRad21 in caspase-3-deficient MCF-7 breast cancer cells. Apoptosis was induced by treatment of MCF-7 cells with 60 μ M etoposide for 6 h. Cells treated with DMSO (vehicle) served as a control. Whole-cell lysates or lysates from the cytoplasmic and nuclear fractions were electrophoresed on an SDS-6% PAGE gel and subjected to Western blot analysis using hRad21 mAb. Arrows indicate the hRad21 products.

sulting in the production of smaller fragments. In the presence of caspase-7 but not caspase-3, a 95-kDa fragment of hRad21 was also generated, suggesting another caspase site N-terminal to the D²⁷⁹ cleavage site. In the *in vitro* cleavage assay, caspase-3 and -7 failed to generate the 60-kDa hRad21 fragment that accompanies the 64-kDa fragment after induction of apoptosis, suggesting that the cleavage site generating the 60-kDa fragment was not recognized by caspase-3 and -7.

To determine whether caspase-3 is essential for the *in vivo* cleavage of hRad21, we utilized a caspase-3-deficient MCF-7 breast cancer cell line (21). In experiments using etoposide- or tamoxifen-induced apoptosis in MCF-7 cells, hRad21 cleavage products were detected, indicating that caspase-3 was not essential for hRad21 cleavage (Fig. 8) and that a caspase other than caspase-3 can act upon hRad21 to cause cleavage following induction of apoptosis.

hRad21 C-terminal cleavage product promotes apoptosis. A possible role for hRad21 in the induction of apoptosis was first seen in preliminary experiments in which overexpression of hRad21 in Molt4, 293T, and MCF7 cells resulted in apoptotic phenotypes. However, conclusive evidence for the role of cleaved hRad21 in the promotion of apoptosis was obtained by transient transfection of 293T and Molt4 cells with cytomega-

lovirus (CMV) promoter-driven *myc*-tagged mammalian expression plasmids encoding the full-length hRad21 or cDNAs encoding the two cleavage products, hRad21 N-terminal (aa 1 to 279) or hRad21 C-terminal (aa 280 to 631) proteins (Fig. 9 and 10). Analysis of transfected 293T cells by multiple apoptosis assays, including examination of cellular morphology under light microscopy (Fig. 9A) and staining with TUNEL (Fig. 9B), Annexin V (Fig. 9C), and DAPI (Fig. 9D), clearly indicated the ability of the 64-kDa C-terminal hRad21 to induce apoptosis. Quantitative analysis of 293T cells transfected with C-terminal hRad21 plasmids indicated a significant increase ($P < 0.05$) of nuclear degradation in cells transfected with the C-terminal hRad21 compared with that in cells transfected with vector control (pCS2MT), WT hRad21 (pCS2MT Rad21), or N-terminal hRad21 (pCS2MT hRad21 N-term) (Fig. 10A). In these cells, apoptosis was also assayed by monitoring the phenotype of the DAPI-stained nuclei. As shown in Fig. 9D, cells transfected with hRad21 C-terminal plasmid displayed significantly more ($P < 0.05$) cellular and nuclear phenotypes typical of apoptosis, such as a round shape with shrunken cell volume, chromatin condensation, and nuclear disintegration, compared with the vector control and cells expressing the full-length and N-terminal hRad21 constructs. Similar results were also obtained with MCF7 and Molt4 cells (data not shown).

The proapoptotic activity of the C-terminal hRad21 was further strengthened by a significantly increased level ($P < 0.05$) of caspase-3 activity in Molt4 cells transfected with hRad21 C-terminal plasmids compared with that in cells transfected with the WT hRad21 (pCS2MT hRad21) and N-terminal hRad21 (pCS2MT hRad21 N-term) constructs. As shown in Fig. 10B, C-terminal hRad21 overexpression resulted in a five- to sevenfold increase in caspase-3 activity compared with that of the empty vector control. Although overexpression of WT hRad21 induced moderate but statistically insignificant levels of apoptosis, as determined by caspase-3 activity in Molt4 cells, overexpression of the hRad21 C-terminal cleavage product but not the N-terminal hRad21 cleavage product dramatically increased caspase-3 activity ($P < 0.05$) in Molt4 cells (Fig. 10B). The transfection efficiency in Molt4 cells was 35%, as determined by cotransfection with a red fluorescence plasmid, pDSRed1-mito. Similar results for caspase-3 activity were also obtained with MCF-7 and 293T cells transfected with hRad21 constructs (data not shown).

Further experiments using vectors to direct hRad21 expression either to the cytoplasm or nucleus demonstrated that expression of hRad21 in the cytoplasm but not in the nucleus resulted in the cleavage of hRad21 protein and induction of apoptosis, as determined by assaying of caspase-3 activity (Fig. 11). It is interesting that both the *myc*-tagged (cytoplasmic) hRad21 and the WT (normally nuclear) hRad21 were cleaved in the cells transiently transfected with the pCMV/*myc*/cyto-hRad21 construct (Fig. 11). In summary, the C-terminal hRad21 cleavage product was proapoptotic, as determined by increased caspase-3 activity and apoptotic morphology, and its translocation to the cytoplasm may play a role in promoting apoptosis. These findings demonstrate the ability of the 64-kDa Rad21 fragment to induce apoptosis.

Apoptotic cleavage of hRad21 is not affected by the status of the p53 tumor suppressor protein in the cell. In view of the pivotal role of the p53 gene product in regulation of the cell

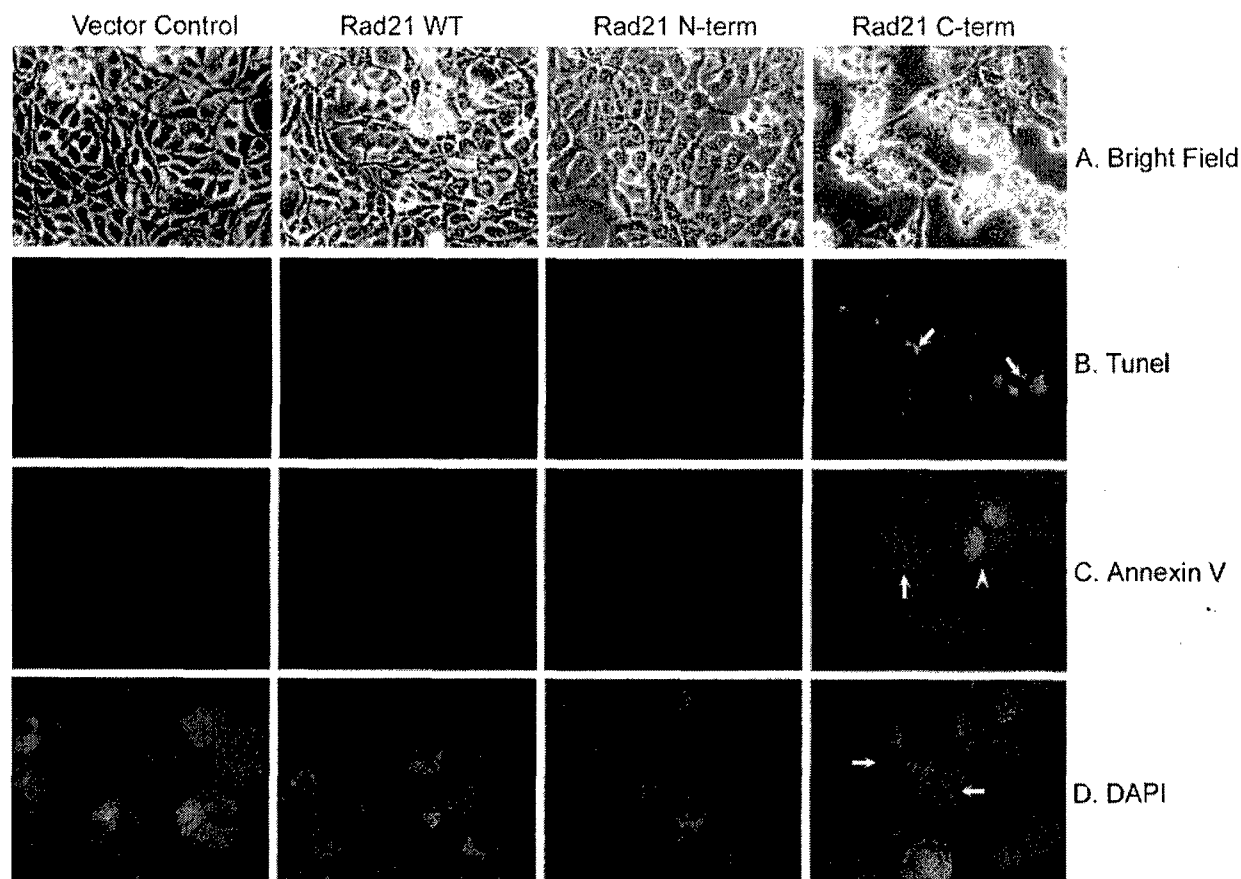


FIG. 9. Analysis of the proapoptotic activity of C-terminal hRad21 in 293T cells by examination of cellular morphology (A) and staining with TUNEL (B), Annexin V (C), and DAPI (D). In panels A to C, 293T cells were transiently transfected with CMV promoter-driven *myc*-tagged mammalian expression plasmids (pCS2MT) encoding the full-length hRad21 or cDNAs encoding the two cleavage products, hRad21 N-terminal (aa 1 to 279) and hRad21 C-terminal (aa 280 to 631) proteins. In panel D, in addition to the above constructs, cells were also cotransfected with a red fluorescence plasmid (pDsRed1-Mito) to account for the hRad21-transfected cells. Note that C-terminal-hRad21-transfected cells have round morphology, as shown in light micrographs (A) and are positive for TUNEL (B) and Annexin V (C) staining (arrows). PI was used to detect the integrity of cell membranes in Annexin V-FITC staining; hence, the nuclei of some apoptotic cells were red (arrowhead). In panel D, more than 50% of the C-terminal-hRad21-transfected cells with red fluorescence have fragmented nuclei and condensed chromatin, typical of apoptotic cells.

cycle and apoptosis, we examined the role of p53 in the apoptotic cleavage of hRad21. We used two myeloid leukemia cell lines, ML-1 and HL-60, with WT and null p53 genotypes, respectively (32, 41). Apoptosis was induced using UV (20 J/m²) and ionizing radiation (20 Gy) in these cells. As shown in Fig. 12, the induction of apoptosis resulted in the cleavage of hRad21 protein in both cell lines, indicating the lack of a role for p53 in hRad21 cleavage.

DISCUSSION

Sister chromatid cohesion during DNA replication plays a pivotal role in accurate chromosomal segregation in the eukaryotic cell cycle. Rad21 is one of the major cohesin subunits that keeps sister chromatids together until anaphase when proteolytic cleavage by separase allows the chromosomes to separate. Mitotic cleavage sites in Rad21 in yeast as well as in humans have been mapped (12, 37, 39). Here we show that hRad21 cleavage occurs during apoptosis and is induced by

various agents, including DNA-damaging (ionizing radiation and topoisomerase inhibitors) and non-DNA-damaging agents (cycloheximide treatment, cytokine withdrawal, and treatment with proteasome inhibitors). We have biochemically mapped the apoptotic cleavage site in human Rad21 (PDSPD²⁷⁹/S), which is distinct from the mitotic cleavage sites (DRE-IMR¹⁷²/E and IEEPSR⁴⁵⁰/L) previously described (12). The apoptotic cleavage site is conserved among vertebrate species, and it is likely that cleavage is mediated by a nuclear caspase or caspase-like molecule, as this cleavage site bears the characteristic caspase-3 subfamily recognition motif (DXXD) and hRad21 is cleaved in vitro by the two major apoptosis executioner caspases, caspase-3 and caspase-7. hRad21 cleavage is not restricted to transformed cancer cells, as induction of apoptosis resulted in hRad21 cleavage in the primary cell line IMR90 (data not shown) as well as the nontransformed immortal cell line EL-12.

Cleavage of hRad21 appears to be an early event in the apoptotic pathway. The immunofluorescence experiments and

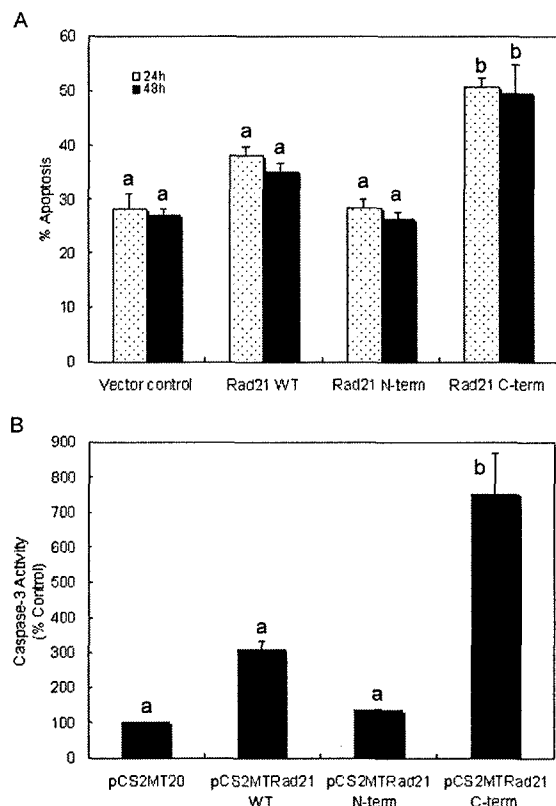


FIG. 10. Quantitative analysis of the proapoptotic activity of C-terminal hRad21 in 293T and Molt4 T-cell leukemia cells. Cells were transiently transfected with CMV promoter-driven *myc*-tagged mammalian expression plasmids encoding the full-length hRad21 or cDNAs encoding the two cleavage products, hRad21 N-terminal (aa 1 to 279) and hRad21 C-terminal (aa 280 to 631) proteins. 293T cells were also cotransfected with the red fluorescence plasmid pDsRed1-mito to account for the hRad21-transfected cells. Nuclear degradation of 293T cells (A) and caspase-3 activity in Molt4 cells (B) were measured as described in Materials and Methods. For the nuclear degradation assay, cells were collected and fixed 24 and 48 h after transfection. The samples were stained with DAPI and examined with fluorescence microscopy. Cells with fragmented nuclei or condensed chromatin were counted as apoptotic. For each sample, a total of 50 intact and degraded nuclei of cells coexpressing pDsRed1-mito (with red fluorescence) was counted. Each data point represents the average and standard errors of the mean from three experiments. The data for caspase-3 activity shown in panel B are the averages and standard errors of the mean from two experiments. The results of the apoptosis assay were analyzed using a binomial test of proportions and those for caspase-3 activity were analyzed using Student's *t* test. Data labeled "a" are significantly different ($P < 0.05$) from data labeled "b."

Western blot analysis of nuclear and cytoplasmic fractions of cells undergoing apoptosis demonstrate the translocation of the hRad21 C-terminal cleavage products to the cytoplasm early (3 to 4 h after insult) in apoptosis. Our results clearly show that hRad21 proteolysis by a caspase family protease at D²⁷⁹/S leads to the production of a proapoptotic C-terminal cleavage product. The specific protease that cleaves hRad21 in vivo and promotes hRad21-induced apoptosis is yet to be identified. Nuclear changes determined by Annexin V staining and examination of the morphology of DAPI-stained nuclei indicate a strong temporal relationship between hRad21 cleavage

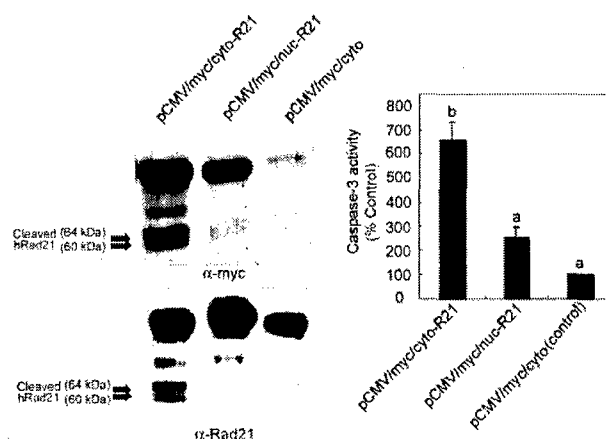


FIG. 11. Effect of the cytoplasmic expression of hRad21 on apoptosis and cleavage of hRad21 protein. Molt4 cells were transiently transfected with the constructs pCMV/*myc*/cyto-hRad21 and pCMV/*myc*/nuc-hRad21, which direct the expression of the recombinant protein to the cytoplasm and nucleus, respectively. Empty pCMV/*myc*/cyto vector served as a control. At 48 h posttransfection, protein lysates were made and subjected to Western blot analysis using c-myc epitope (9E10) and hRad21 mAb to detect the fusion and/or native hRad21 proteins, respectively. Lysates were also used for the assaying of caspase-3 activity as described in Materials and Methods. The data for caspase-3 activity shown at right are the averages and standard errors of the mean from two experiments. Individual values were compared using Student's *t* test, and values labeled "a" are significantly different ($P < 0.05$) from that labeled "b."

and apoptosis. As determined by Annexin V staining, hRad21 cleavage correlates well with the early events of apoptosis when the cell membrane remains intact. Furthermore, the progressive increase in the cleavage of hRad21 correlates well with the level of caspase activation, as determined by assaying of by caspase-3 activity. Translocation of the 64-kDa hRad21 cleavage product to the cytoplasm early in apoptosis may act as a nuclear signal that promotes and accelerates subsequent events of apoptosis. The specificity of this product was determined further, as the N-terminal hRad21 cleavage product neither translocates nor has the ability to induce apoptosis. We have not explored the role of the 60-kDa hRad21 product generated at a cleavage site other than D²⁷⁹/S in the apoptotic process.

The physiological significance of cohesin hRad21 cleavage in apoptosis is intriguing. The nuclear signal(s) that detects subsequent events of apoptosis in the cytoplasm and mitochondria has remained elusive. It is possible that cleavage of hRad21 at the onset of apoptosis and the translocation of the C-terminal cleavage product to the cytoplasm act as cues to accelerate the apoptotic process. Supporting evidence in favor of this possibility include the following: (i) hRad21 is not normally cytoplasmic; (ii) early in apoptosis, hRad21 is found in the cytoplasm; and (iii) directed expression of either the C-terminal or full-length hRad21 to the cytoplasm induces apoptosis. It is not clear whether localization of C-terminal hRad21 to the cytoplasm is due to an active or a passive transport process following cleavage. The carboxy-terminal fragment contains a putative nucleolar localization signal sequence, which argues against a passive transport process. These findings further strengthen the notion that the translocation of the C-terminal

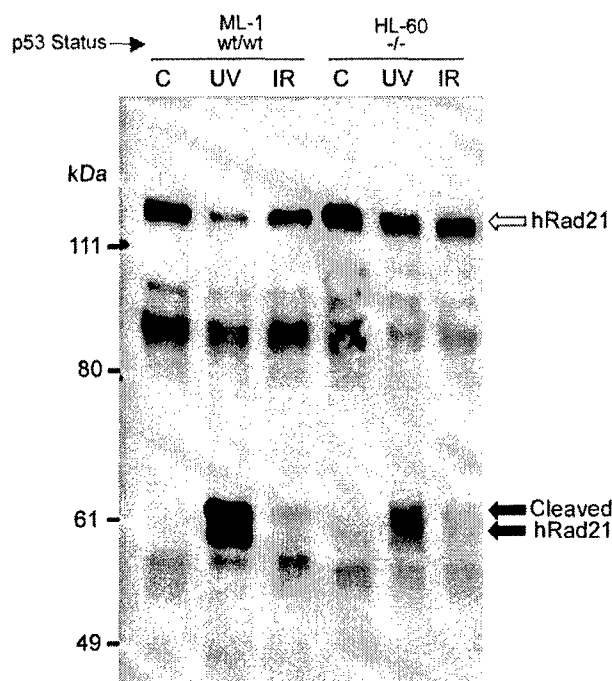


FIG. 12. Effect of p53 status on the cleavage of hRad21. Apoptosis was induced in the myeloid leukemia cell lines ML-1 and HL-60, with WT and null p53 genotypes, respectively, by treatment of the cells with UV light (20 J/m²) or ionizing radiation (IR) (20 Gy). Six hours after treatment, protein lysates were made and resolved by SDS-6% PAGE followed by Western blot analysis using hRad21 mAb. Arrows indicate hRad21 cleavage products. C, control without UV or IR treatment.

hRad21 protein to the cytoplasm may play a functional role in apoptosis.

We have firmly established the proapoptotic activity of the C-terminal hRad21 cleavage product by several apoptotic assays, including Annexin V staining, TUNEL methods, quantitative measurement of DAPI-stained nuclear morphology, and assaying of caspase-3 activity. However, the exact mechanism by which cleaved hRad21 induces apoptosis requires further investigation. It is interesting that a BLAST search of the apoptosis database (www.apoptosis-db.org) indicated that C-terminal hRad21 possesses a stretch of 80 aa (aa 282 to 362) that has homology to the tumor necrosis factor receptor superfamily and other apoptosis-inducing proteins, including TRAIL-R2 and death receptor 5. However, the functional significance of this domain in apoptosis-inducing proteins is not known.

The caspase-mediated proteolysis of hRad21 and the partial removal of hRad21 from the nucleus may also expose the chromosomal DNA to DNase and other proteins responsible for chromatin condensation and apoptotic DNA fragmentation. hRad21 was originally isolated in fission yeast as an essential protein with a role in the repair of DNA double-strand breaks induced by ionizing radiation (2). It is therefore logical to think that disruption of the DNA repair function of hRad21 may be necessary during the execution of apoptosis. This notion has been strengthened by recent findings that a number of DNA repair enzymes such as Rad51 (15), ATM (13), DNA-PK (4), and PARP (22) and cell cycle regulators such as retino-

blastoma protein (9) are cleaved by caspases. Coordinated destruction of the DNA repair machinery and cell cycle regulators by the caspase family of proteases therefore constitutes a physiologically relevant process that promotes and accelerates chromosomal condensation and DNA fragmentation without interference by the cell cycle and DNA repair machinery. Unlike hRad21, however, cleavage products of these other DNA repair proteins have not been reported to play a direct role in promoting apoptosis. In this case, cleavage of hRad21 by caspases may play a unique role in amplifying the apoptotic signal by elevating the level of caspase activity. A similar mechanism for amplifying the apoptotic signal for the caspase substrate vimentin has recently been described (3).

The p53 tumor suppressor protein plays a central role in the regulation of the cell cycle and apoptosis after DNA damage (17, 34). In the event that DNA damage is more severe and not repairable, p53 directs the cells into apoptosis through the Bax/Bcl-2 pathway. p53 status does not appear to have any effect on the apoptotic cleavage of hRad21 after DNA damage (i.e., UV and ionizing radiation), indicating the lack of involvement of the p53 pathway in hRad21 cleavage. It is possible that a parallel p53-independent pathway may regulate the genotoxic-damage-induced cleavage of hRad21.

Finally, it is interesting that cleavage of cohesin hRad21 is carried out by a separase in mitosis and by a caspase in apoptosis at different sites in the protein. Both of these proteases belong to the distantly related CD clan protease family (38), suggesting an evolutionarily conserved mechanism shared by the mitotic and apoptotic machinery. hRad21 may serve as the link between the two key cellular processes of mitosis and apoptosis. In summary, in contrast to the previously described functions of Rad21, i.e., in chromosome segregation and DNA repair, cleavage of the cohesin protein and translocation of the C-terminal cleavage product to the cytoplasm are early events in the apoptotic pathway that amplify the apoptotic signal in a positive-feedback manner, possibly by activating more caspases. These results provide the framework for identification of the physiologic role of hRad21 in the apoptotic response in normal and malignant cells.

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ADDENDUM IN PROOF

A similar conclusion regarding the function of RAD21 in apoptosis has been published by F. Chen et al. (*J. Biol. Chem.* 277:16775-16781, 2002).

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